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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 10:13:38 ; Search time 118 seconds
(without alignments)
7844.560 Million cell updates/sec

Title: US-09-712-338-1
Perfect score: 1668
Sequence: 1 atggctggctacgaattctt.....ccagtgttgatgcatag 1668

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1662	99.6	1662	3	US-08-943-714-1
2	86.4	5.2	2503	1	US-09-640-305-3
3	86.4	5.2	2503	1	US-08-360-673-3
4	84	5.0	2002	1	US-08-309-341-3
5	84	5.0	2002	1	US-08-608-267-3
6	84	5.0	2002	1	US-08-608-452-3
7	84	5.0	2002	1	US-08-608-224-3
8	84	5.0	2002	2	US-08-967-149-3
9	76	4.6	2068	1	US-08-309-341-1
10	76	4.6	2068	1	US-08-608-267-1
11	76	4.6	2068	1	US-08-608-452-1
12	76	4.6	2068	1	US-08-608-224-1
13	76	4.6	2068	2	US-08-967-149-1
14	66.2	4.0	2632	3	US-08-899-324-32
15	66.2	4.0	2632	3	US-08-329-892B-32
16	56.4	3.4	1814	4	US-09-702-705-319
17	56.4	3.4	1814	4	US-09-736-457-319
18	56.4	3.4	1814	4	US-09-614-124B-319
19	56.4	3.4	1814	4	US-09-671-125-319
20	56.4	3.4	1814	4	US-09-589-184-319
21	47.6	2.9	390	3	US-09-197-649-7
22	47.6	2.9	1551	2	US-08-828-488-4
23	47.6	2.9	1551	4	US-09-299-689A-4
24	47.6	2.9	2076	4	US-09-907-794A-163
25	47.6	2.9	2076	4	US-09-905-125A-163
26	47.6	2.9	2076	4	US-09-902-775A-163
27	47.2	2.8	1670	2	US-08-828-488-2

ALIGNMENTS

RESULT 1

US-08-943-714-1

; Sequence 1, Application US/08943714

; Patent No. 6187578

; GENERAL INFORMATION:

; APPLICANT: Blinkovsky, Alexander

; APPLICANT: Berka, Randy

; APPLICANT: Rev, Michael

; APPLICANT: Golightly, Elizabeth

; APPLICANT: Klotz, Alan

; APPLICANT: Mathisen, Thomas Erik

; APPLICANT: Dammann, Claus

; TITLE OF INVENTION: Carboxypeptidases And Nucleic Acids

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 61875780 No. 6187578disk of No. 6187578th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,714

; FILING DATE: 03-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4990.200-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1662 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1..1662

; OTHER INFORMATION:

Sequence 2, Appli
Sequence 674, App
Sequence 131, App
Sequence 18033, A
Sequence 11967, A
Sequence 8154, Ap
Sequence 11893, A
Sequence 8222, Ap
Sequence 11930, A
Sequence 8276, Ap
Sequence 8046, Ap
Sequence 35, Appl
Sequence 51, Appl
Sequence 2, Appl
Sequence 10938, A
Sequence 11178, A
Sequence 11076, A
Sequence 173, App

28 47.2 2.8 1670 4 US-09-299-689A-2
29 45.4 2.7 1071 4 US-09-023-655-674
30 39.8 2.4 357 4 US-09-280-116-131
31 38.8 2.3 474 4 US-09-621-976-18033
32 38.6 2.3 447 4 US-09-252-991A-11967
33 38.6 2.3 630 4 US-09-252-991A-8154
34 38.6 2.3 774 4 US-09-252-991A-11893
35 38.6 2.3 777 4 US-09-252-991A-8222
36 38.6 2.3 1083 4 US-09-252-991A-11930
37 38.6 2.3 1239 4 US-09-252-991A-8276
38 38.6 2.3 1434 4 US-09-252-991A-8046
39 38.2 2.3 918 3 US-09-105-390-35
40 38.2 2.3 1008 3 US-09-105-390-51
41 38.2 2.3 1949 3 US-09-105-390-2
42 37.2 2.2 870 4 US-09-252-991A-10938
43 37.2 2.2 1785 4 US-09-252-991A-11178
44 37.2 2.2 2091 4 US-09-252-991A-11076
45 36.8 2.2 7012 4 US-09-221-017B-173

APPLICATION NUMBER: US/08/360,673
FILING DATE: 06-FEB-1995
APPLICATION NUMBER: WO PCT/FR93/00623
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: FR 92/07785
FILING DATE: 25-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST92040-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Kluyveromyces lactis
FEATURE:
NAME/KEY: CDS
LOCATION: 387..1862
OTHER INFORMATION: /product= "K. lactis protease C
gene"
/gene= "K1.PRC1"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-640-305-3

Query Match 5.2%; Score 86.4; DB 1; Length 2503;
Best Local Similarity 57.4%; Pred. No. 6.8e-16;
Matches 156; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 199 GTCAAATCCTACTCTGGATATGTCGACACCTCTCCCGAGTCCCATACCTCTTCTTCTGTTTC 258
DB 624 GTGAACAATGTCGGGATATTAGATTACCGAGCTCAAAACACTCTTTTATTGGTTT 683
QY 259 TTCGAAGCCAGACATACCCAGAACTGCACCTATCAGATTGTGTTGAATGGTGGCCCT 318
DB 684 TTGAGCTGAAGATGACCCAGAGAAATGACCCAGTACTATGTTGTTAAACGGTGGTCT 743
QY 319 GGAAGCGATTCTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCCATGTCATTCGACT 378
DB 744 GGCTGTTCTCTTTCGTCGGTCTTTCTTTGAATTGGACCTTCTCTATAGGAGCTGAT 803
QY 379 TTTGATGACTACATCAACCCCTCCTCGTGGAAACGAGGTCTCCAAATTTACTATTCTGTCC 438
DB 804 TTGAACCCATTATTAACCCCTACTCTTGGAAATCCAAAGCTTCTGTGATATTCCTAGAT 863
QY 439 CAGCCATTGGAGTCGGCTTTTCATATAGTGA 470
DB 864 CAGCCTGTGGTGTGGGTTCTCATACGGTGA 895

RESULT 3
US-08-360-673-3
Sequence 3, Application US/08360673
Patent No. 5679544
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: MODIFIED KLUYVEROMYCES YEASTS, THEIR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA

ZIP: 19002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,673
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/FR93/00623
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/07785
FILING DATE: 25-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST92040-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Kluyveromyces lactis
FEATURE:
NAME/KEY: CDS
LOCATION: 387..1862
OTHER INFORMATION: /product= "K. lactis protease C
gene"
OTHER INFORMATION: /gene= "K1.PRC1"
US-08-360-673-3

Query Match 5.2%; Score 86.4; DB 1; Length 2503;
Best Local Similarity 57.4%; Pred. No. 6.8e-16;
Matches 156; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 199 GTCAAATCCTACTCTGGATATGTCGACACCTCTCCCGAGTCCCATACCTCTTCTTCTGTTTC 258
DB 624 GTGAACAATGTCGGGATATTAGATTACCGAGCTCAAAACACTCTTTTATTGGTTT 683
QY 259 TTCGAAGCCAGACATACCCAGAACTGCACCTATCAGATTGTGTTGAATGGTGGCCCT 318
DB 684 TTGAGCTGAAGATGACCCAGAGAAATGACCCAGTACTATGTTGTTAAACGGTGGTCT 743
QY 319 GGAAGCGATTCTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCCATGTCATTCGACT 378
DB 744 GGCTGTTCTCTTTCGTCGGTCTTTCTTTGAATTGGACCTTCTCTATAGGAGCTGAT 803
QY 379 TTTGATGACTACATCAACCCCTCCTCGTGGAAACGAGGTCTCCAAATTTACTATTCTGTCC 438
DB 804 TTGAACCCATTATTAACCCCTACTCTTGGAAATCCAAAGCTTCTGTGATATTCCTAGAT 863
QY 439 CAGCCATTGGAGTCGGCTTTTCATATAGTGA 470
DB 864 CAGCCTGTGGTGTGGGTTCTCATACGGTGA 895

RESULT 4
US-08-309-341-3
Sequence 3, Application US/08309341
Patent No. 5594119
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER

Patent No. 5693510
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56935100 No. 5693510disk of No. 5693510th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,452
FILING DATE: 28-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 349..411
FEATURE:
NAME/KEY: CDS
LOCATION: join (348..412)
US-08-608-452-3

Query Match 5.0%; Score 84; DB 1; Length 2002;
Best Local Similarity 55.5%; Pred. No. 3.3e-15;
Matches 161; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 223 GACACCTCTCCGAGTCCCATACCTCTCTGTTCTTCGAAAGCCAGACATACCCAGAA 282
Db 617 GACAAACGAGAACGACAAAGCATCTCTCTGTTCTTCGAGTCTCGCAATGACCCGAG 676
QY 283 ACTGCACCTATCATGTTGGTTGAATGGTGGCCCTGGAAGCGATTCTTTGATCGGTCTC 342
Db 677 AATGACCCCTGTGTTCTGTTGCTGAACCGTGGCCCTGGATGCTCTTCCCTCACCGTCTT 736
QY 343 TTCGAAGAGTTGGCCCTTCGCATGTCAATTCGACTTTTGTATGACTACATCAACCCCTAC 402
Db 737 TTATGAGGCTCGGCCCTAGCAGCATCAACAGAGATCAGCCGGTCTCAACGACTAC 796
QY 403 TCGTGAACGAGGTCTCCAAATTTACTATTCTGTCAGGCAATGGGAGTCGGCTTTTCA 462
Db 797 GCTTGAACCTCAACGCGTCCGTGATCTCTCTTGACCCAGCGCTGCAACGTCGGTACTCT 856
QY 463 TATAGTATACGGTTGATGGTCCATTAACCTGTAACTGGGGTCTGTCGA 512
Db 857 TACAGCAACTCTGCTGTGTCAGCAGACACCGTTGCTGCTGGCAGGACGTCTA 906

RESULT 7
US-08-608-224-3
Sequence 3, Application US/08608224
Patent No. 5705376
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57053760 No. 5705376disk of No. 5705376th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,224
FILING DATE: 28-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 349..411
FEATURE:
NAME/KEY: CDS
LOCATION: join (348..412)
US-08-608-224-3

Query Match 5.0%; Score 84; DB 1; Length 2002;
Best Local Similarity 55.5%; Pred. No. 3.3e-15;
Matches 161; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 223 GACACCTCTCCGAGTCCCATACCTCTCTGTTCTTCGAAAGCCAGACATACCCAGAA 282
Db 617 GACAAACGAGAACGACAAAGCATCTCTCTGTTCTTCGAGTCTCGCAATGACCCGAG 676
QY 283 ACTGCACCTATCATGTTGGTTGAATGGTGGCCCTGGAAGCGATTCTTTGATCGGTCTC 342
Db 677 AATGACCCCTGTGTTCTGTTGCTGAACCGTGGCCCTGGATGCTCTTCCCTCACCGTCTT 736
QY 343 TTCGAAGAGTTGGCCCTTCGCATGTCAATTCGACTTTTGTATGACTACATCAACCCCTAC 402
Db 737 TTATGAGGCTCGGCCCTAGCAGCATCAACAGAGATCAGCCGGTCTCAACGACTAC 796
QY 403 TCGTGAACGAGGTCTCCAAATTTACTATTCTGTCAGGCAATGGGAGTCGGCTTTTCA 462
Db 797 GCTTGAACCTCAACGCGTCCGTGATCTCTCTTGACCCAGCGCTGCAACGTCGGTACTCT 856

QY 373 TCGACTTTTGATGACTACATCAACCCCTCACTCGTGAACGAGGTCTTCCAAATTTACTATTC 432
 Db 753 AAGAAGATCCAGCGGTCTTACAAATGACTAGTGGTTCGAACTCCAAAGCGTCCGTGATCTTC 812
 QY 433 CTGTCCAGCCATTGGAGTGGCTTTTCATATAGTGAATACGGTTGATGGGTCCATTAAC 492
 Db 813 CTGTACCAAGCGTGTCAATGTGGTGTACTCTTACAGTAAGTCTGTCTGTGAGCGACACGGTC 872
 QY 493 CCGTGAACCTGGGTGGTCTGCGA 512
 Db 873 GCTGTGGAAGGACGTCTA 892

RESULT 10
 US-08-608-267-1
 ; Sequence 1, Application US/08608267
 ; Patent No. 5688663
 ; GENERAL INFORMATION:
 ; APPLICANT: Yaver, Debbie Sue
 ; APPLICANT: Thompson, Sheryl Ann
 ; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 56886630 No. 56886630 disk of No. 56886630th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/608,267
 ; FILING DATE: 28-FEB-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/309,341
 ; FILING DATE: 20-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney, Karen A.
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 4247.000-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2068 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: intron
 ; LOCATION: 572..632
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join (571..633)
 ; US-08-608-267-1

Query Match 4.6%; Score 76; DB 1; Length 2068;
 Best Local Similarity 55.8%; Pred. No. 8.9e-13;
 Matches 145; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
 QY 253 TGGTCTTCGAGCCACACATCAACCCGAGAACTGCACCTATCATATGTTGGTGAATGTT 312
 Db 633 TGGTCTTCGAGTCTCGAATGACCCCGAGAAATGATCCCGTGTCTGTGCTGCTGAACGGT 692

QY 313 GGCCCTGGAAGGATCTTTGATCGGTCTTTCGGAAGAGTGGGCGCTTGGCATGTCAT 372
 Db 693 GGCCCTGGGTGCTCTTCCCTCACCCTGCTCTTTCATGAGCTTGGCCCTAGCAGCATCAAC 752
 QY 373 TCGACTTTTGATGACTACATCAACCCCTCACTCGTGAACGAGGTCTTCCAAATTTACTATTC 432
 Db 753 AAGAAGATCCAGCGGTCTTACAAATGACTAGTGGTTCGAACTCCAAAGCGTCCGTGATCTTC 812
 QY 433 CTGTCCAGCCATTGGAGTGGCTTTTCATATAGTGAATACGGTTGATGGGTCCATTAAC 492
 Db 813 CTGTACCAAGCGTGTCAATGTGGTGTACTCTTACAGTAAGTCTGTCTGTGAGCGACACGGTC 872
 QY 493 CCGTGAACCTGGGTGGTCTGCGA 512
 Db 873 GCTGTGGAAGGACGTCTA 892

RESULT 11
 US-08-608-452-1
 ; Sequence 1, Application US/08608452
 ; Patent No. 5693510
 ; GENERAL INFORMATION:
 ; APPLICANT: Yaver, Debbie Sue
 ; APPLICANT: Thompson, Sheryl Ann
 ; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 56935100 No. 56935100 disk of No. 56935100th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/608,452
 ; FILING DATE: 28-FEB-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/309,341
 ; FILING DATE: 20-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney, Karen A.
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 4247.000-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2068 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: intron
 ; LOCATION: 572..632
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join (571..633)
 ; US-08-608-452-1

Query Match 4.6%; Score 76; DB 1; Length 2068;
 Best Local Similarity 55.8%; Pred. No. 8.9e-13;
 Matches 145; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 253 TGGTCTTCGAAGCAGACATAACCCAGAACTGCACCTATCACATTCTGGTTGAATGGT 312
DB 633 TGGTCTTCGAAGTCTCGCAATGACCCCGAAGATGATCCCGTGTCTGTGGCTGAACGGT 692
QY 313 GGCCCTCGAAGCGATTCTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCCTATCTCAAT 372
DB 693 GGCCCTGGGTGCTCTTCCTCTACCGGTCTCTTCATGGAGCTTGGCCCTAGCAGCATCAAC 752
QY 373 TCGACTTTTGATGACTACATCAACCCCTCACTCGTGGAAAGAGGTCTCCAAATTTACTATTC 432
DB 753 AAGAGATCCAGCGGTCTTACAAATGACTACCGTCTGGAATCCCAACGGCTCCGTGATCTTC 812
QY 433 CTGTCCCGACCATTTGGAGTGGCTTTTCATATAGTATACGGTTGATGGGTCCCAATTAAC 492
DB 813 CTGTGACCAAGCGTCTCAATGTCGGTTACTCTCTACAGTAATCTCTGCTGTCAGCAGCGTCT 872
QY 493 COTGTAACTGGGTGCTGCGA 512
DB 873 GCTGCTGGCAAGGACGTCTA 892

RESULT 12

US-08-608-224-1
; Sequence 1, Application US/08608224
; Patent No. 5705376
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5705376o No. 5705376disk of No. 5705376th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/608,224
; FILING DATE: 28-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-608-224-1

Query Match 4.6%; Score 76; DB 1; Length 2068;
Best Local Similarity 55.8%; Pred. No. 8.9e-13;
Matches 145; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
QY 253 TGGTCTTCGAAGCAGACATAACCCAGAACTGCACCTATCACATTCTGGTTGAATGGT 312
DB 633 TGGTCTTCGAAGTCTCGCAATGACCCCGAAGATGATCCCGTGTCTGTGGCTGAACGGT 692
QY 313 GGCCCTCGAAGCGATTCTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCCTATCTCAAT 372
DB 693 GGCCCTGGGTGCTCTTCCTCTACCGGTCTCTTCATGGAGCTTGGCCCTAGCAGCATCAAC 752
QY 373 TCGACTTTTGATGACTACATCAACCCCTCACTCGTGGAAAGAGGTCTCCAAATTTACTATTC 432
DB 753 AAGAGATCCAGCGGTCTTACAAATGACTACCGTCTGGAATCCCAACGGCTCCGTGATCTTC 812
QY 433 CTGTCCCGACCATTTGGAGTGGCTTTTCATATAGTATACGGTTGATGGGTCCCAATTAAC 492
DB 813 CTGTGACCAAGCGTCTCAATGTCGGTTACTCTCTACAGTAATCTCTGCTGTCAGCAGCGTCT 872
QY 493 COTGTAACTGGGTGCTGCGA 512
DB 873 GCTGCTGGCAAGGACGTCTA 892

RESULT 13

US-08-967-149-1
; Sequence 1, Application US/08967149
; Patent No. 5939305
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF
; TITLE OF INVENTION: ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939305o No. 5939305disk of No. 5939305th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,149
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,452
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:


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; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-967-149-1

Query Match
Best Local Similarity 4.6%; Score 76; DB 2; Length 2068;
Matches 145; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 253 TGGTCTTCGAGCCAGACATTAACCCAGAACTGCACTTATCACATTTGGTTGAATGTT 312
Db |||||
QY 633 TGGTCTTCGAGCTCGCAATGACCCGAGAAATGATCCGTTGTTCTGTGGCTGAAGGT 692
Db |||||
QY 313 GGCCTCGGAAGGATTTCTTGTATCGTCTCTTCGAAGAGTTGGGCCCTTGCCATGCAAT 372
Db |||||
QY 693 GGCCTCGGAGTCTCTTCCCTACCGGCTCTTCATGGAGCTTGGCCCTAGCAGCATCAAC 752
Db |||||
QY 373 TCGACTTTTGATGACTACATCAACCTCACTCGTGGAAACGAGGTCTCCAAATTTACTATT 432
Db |||||
QY 753 AAGAGATCCAGCGGTCTACAATGACTACGCTTGGAACTCCAAAGCGTCCGTGATCTTC 812
Db |||||
QY 433 CTGTCCCGAGCCATTTGGAGTGGCTTTTCATATAGTATGATCGTTGATGGGTCCATTAAC 492
Db |||||
QY 813 CTTGACCAAGCCTGCTCAATGTGCGTTACTCTACAGTAATCTCTGCTGTCAGCGACACGTC 872
Db |||||
QY 493 CCTGTAACTGGGCTGCTCGA 512
Db |||||
QY 873 GCTGCTGCAAGGACGTCTA 892
Db |||||
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RESULT 14
US-08-899-324-32
; Sequence 32, Application US/08899324
; Patent No. 5945329
; GENERAL INFORMATION:
; APPLICANT: Breddam, Klaus
; APPLICANT: Keilland-Brandt, Morten
; APPLICANT: Mortensen, Uffe
; APPLICANT: Olesen, Kjeld
; APPLICANT: Stenmick, Henning
; APPLICANT: Wagner, Fred
; TITLE OF INVENTION: CUSTOMIZED PROTEASES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5945329west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,324
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/329,892
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: 08/144,704
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettleberger, Denise M
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 8648.44USCI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
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; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 696...2291
; OTHER INFORMATION:
US-08-899-324-32

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Best Local Similarity 4.0%; Score 66.2; DB 2; Length 2632;
Matches 140; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 1113 CATTCCTTCTTGGACTTTTGAAGTAGAAACGATCTCTGCAAGGATCCGGTCACTCTT 1172
Db |||||
QY 301 TGGTTGAATGTTGGCCCTGGAAGCGATTTCTTTGATGCGTCTCTTCGAAGAGTTGGGCCCT 360
Db |||||
QY 1173 TGGTTGAAGCGGGTCCAGGTTGTTCTTCACTAACCGGGCTGTTCTTTTGAATTAGGACCC 1232
Db |||||
QY 361 TGCCATGTCATTCGACTTTTGTATGACTACATCACTCACTCACTCGGAAACCCATCGGAAACCC 420
Db |||||
QY 1233 TCATCCATGGAACCTGATTTTGAACCCATCGGAAACCCATCGGAAACCCATCGGAAACCC 1292
Db |||||
QY 421 AATTACTATTCTCTGTCGCCAGCCATTTGGAGTCCGGCTTTTCATATAGTATGATACGGTTGAT 480
Db |||||
QY 1293 ACCGTGATCTCTTGTGACCGCTGTCAACGTTGGGTTCTGTTATTCGGGTCTCTCAGGT 1352
Db |||||
QY 481 GGGTCCATTAACCTGTAACCTGG 503
Db |||||
QY 1353 GTTCCCAACACTGTCGCGCTGG 1375
Db |||||

RESULT 15
US-08-329-892B-32
; Sequence 32, Application US/08329892B
; Patent No. 6187579
; GENERAL INFORMATION:
; APPLICANT: Breddam, Klaus
; APPLICANT: Keilland-Brandt, Morten
; APPLICANT: Mortensen, Uffe
; APPLICANT: Olesen, Kjeld
; APPLICANT: Stenmick, Henning
; APPLICANT: Wagner, Fred
; TITLE OF INVENTION: CUSTOMIZED PROTEASE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6187579west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,892B
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/144,704
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettleberger, Denise M
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 8648.44US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 696...2291
; OTHER INFORMATION:
;
US-08-329-892B-32

Query Match 4.0%; Score 66.2; DB 3; Length 2632;
Best Local Similarity 53.2%; Pred. No. 9.4e-10;
Matches 140; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 241 CATACCTTCTTGGTTCTTCGAGCCAGACATACCCAGAACTGCACCTATCACATTG 300
DB 1113 CATTCTCTTTGGACTTTGAAAGTAGAAACGATCTCGAAAGGATCCGGTCATCCTT 1172

QY 301 TGGTTGAATGGTGGCCCTCGAAGCGATTCTTTGATCGGTCTCTTCGAAGAGTTGGGCCCT 360
DB 1173 TGGTTGAACGGGGTCCAGGTGTTCTTCACTAACGGGGTGTCTTTGAATTAGGACCC 1232

QY 361 TGCATGTCAATTCGACTTTTATGATGATCATCAACCCCTCACTCGTGGAAACGAGGTCTCC 420
DB 1233 TCATCCATTGGACCTGATTGAAACCCATCGGGAACCCCTTACTCTTTGGAACAGCAATGCC 1292

QY 421 AATTACTATTCTGTCCAGCCATTGGGAGTCGGCTTTTCATATAGTATAGCGTTGAT 480
DB 1293 ACCGTGATCTTCTTGACCAAGCCTGTCAACGTTGGGTCTCTGATTTCCGGGTCCTCAGGT 1352

QY 481 GGGTCCATTAAACCCGTAACTGG 503
DB 1353 GTTCCACACTGTCGCCGCTGG 1375
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Job time : 120 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 11:28:14 ; Search time 791 Seconds
(without alignments)
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Title: US-09-712-338-1

Perfect score: 1668

Sequence: 1 atgcgtggctacgaattctt.....ccagtggtgtagcatag 1668

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374.8	22.5	1859	16	US-10-369-493-36581 Sequence 36581, A
2	91.6	5.5	1686	16	US-10-369-493-27042 Sequence 27042, A
3	70.6	4.2	2218	13	US-09-993-192-1 Sequence 1, Appli
4	70.6	4.2	2218	15	US-10-206-619-1 Sequence 1, Appli
5	67	4.0	1619	16	US-10-369-493-27598 Sequence 27598, A
6	66.2	4.0	1599	16	US-10-369-493-25613 Sequence 25613, A
7	65.6	3.9	1289	16	US-10-369-493-36920 Sequence 36920, A
8	61.8	3.7	1527	16	US-10-369-493-25156 Sequence 25156, A
9	56.4	3.4	1814	9	US-09-736-457-319 Sequence 319, App
10	56.4	3.4	1814	9	US-09-902-941-319 Sequence 319, App
11	56.4	3.4	1814	9	US-09-849-626-319 Sequence 319, App
12	56.4	3.4	1814	10	US-09-476-300-319 Sequence 319, App
13	56.4	3.4	1814	13	US-10-283-017-319 Sequence 319, App
14	56.4	3.4	1814	15	US-10-017-754-319 Sequence 319, App

15	56.4	3.4	1814	15	US-10-113-872-319	Sequence 319, App
16	56.4	3.4	1815	9	US-09-880-107-2296	Sequence 2296, Ap
17	56.4	3.4	1815	17	US-10-450-826-69	Sequence 69, Appl
18	55.8	3.3	710	16	US-10-369-493-29440	Sequence 29440, A
19	54.8	3.3	2864	9	US-09-925-302-331	Sequence 331, App
20	54.8	3.3	2864	13	US-09-925-302-331	Sequence 331, App
21	53.4	3.2	1503	17	US-10-437-963-97753	Sequence 97753, A
22	53.2	3.2	1383	17	US-10-437-963-62737	Sequence 62737, A
23	52.6	3.2	1514	13	US-10-425-114-29826	Sequence 29826, A
24	52.6	3.2	1905	13	US-10-424-599-104947	Sequence 104947, A
25	51.2	3.1	1326	16	US-10-369-493-27091	Sequence 27091, A
26	49	2.9	1113	16	US-10-369-493-36625	Sequence 36625, A
27	49	2.9	1574	13	US-10-425-114-6508	Sequence 6508, Ap
28	49	2.9	1717	13	US-10-424-599-132435	Sequence 132435, A
29	47.6	2.9	390	9	US-09-790-399-7	Sequence 7, Appli
30	47.6	2.9	1551	14	US-10-084-018-4	Sequence 4, Appli
31	47.6	2.9	1684	9	US-09-729-674-109	Sequence 109, App
32	47.6	2.9	1697	10	US-09-796-753-39	Sequence 39, Appl
33	47.6	2.9	1949	10	US-09-971-429B-33	Sequence 33, Appl
34	47.6	2.9	1963	13	US-10-296-115-586	Sequence 586, App
35	47.6	2.9	2076	9	US-09-909-320-163	Sequence 163, App
36	47.6	2.9	2076	9	US-09-909-088B-163	Sequence 163, App
37	47.6	2.9	2076	9	US-09-905-291A-163	Sequence 163, App
38	47.6	2.9	2076	9	US-09-902-853-163	Sequence 163, App
39	47.6	2.9	2076	9	US-09-907-824-163	Sequence 163, App
40	47.6	2.9	2076	9	US-09-907-841-163	Sequence 163, App
41	47.6	2.9	2076	10	US-09-904-011-163	Sequence 163, App
42	47.6	2.9	2076	10	US-09-906-742-163	Sequence 163, App
43	47.6	2.9	2076	10	US-09-906-838-163	Sequence 163, App
44	47.6	2.9	2076	10	US-09-907-613-163	Sequence 163, App
45	47.6	2.9	2076	10	US-09-907-942-163	Sequence 163, App

ALIGNMENTS

RESULT 1

US-10-369-493-36581
; Sequence 36581, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36581
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-369-493-36581

Query Match 22.5%; Score 374.8; DB 16; Length 1859;
Best Local Similarity 58.0%; Pred. No. 3.2e-114;
Matches 1067; Conservative 0; Mismatches 402; Indels 371; Gaps 8;

QY	76	TCGTCGGTAGAAGACAGCTCCCAAGAACCCACCGGGGTCAAGACTCTTACACCGCA	135
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QY	136	ACAATGTCCATCCGTTACAGGAACCCGGGGCAGAGGGGTCTGCGAGACTACCCCG	195
Db	79	AATGGTGTGACCATCGATACAGAGGAGCTGGTAAGAGGGTGTCTGTGAGAGCCCT	138
QY	196	GGTGTCAATCTACTCTCGATATGCGACACCTCTCCGAGTCCCATACCTTCTTCTGG	255

Db 139 GGTGTCAACTCTTATCTCGATACGTTGATCTATCGCTGAGTCTCACACCTTCTTTTAC 198
QY 256 TTCTTGAAGCAGACATAACCCAGAACTGCACCTATCACATGTGTGTTGAATGGTGGC 315
Db 199 TTCTTGAAGCTGCTCATGACCCGCAACGCTCTATCACTCTGTGGCTGAATGGTGGC 258
QY 316 CTTGGAAGCGATTTCTTGTATCGGTCTCTTGA 347
Db 259 CCGGAAGTGATTCGTTATCGGGCTTTTGAAGGTTTGTACTGCTGACTGGGTTACAA 318
QY 348 -----AGATTGGGCCCTTGGCCATGTCATGTCATTCGACTT 379
Db 319 GAAGTGTGATGACTGATGGGCTTCTTTAGAACTGGGACCGTCTATCAGGAGAACC 378
QY 380 TTGATGACTACATCAACCTCTCACTCGTGAACGAGGTCTCCAAATTTACTATTCTCTGTGCC 439
Db 379 TGACGACCTACGTCAACCATACTCGTGAATGAAGTCTCCAACTTTTGTTCATCTGCG 438
QY 440 AGCCATTTGGAGTC-----ATA 574
Db 439 AGCCATTTGGAGTCGATGAGGAATTTGTGTTTGTGTCGTCAGCTTCTCACTGG 498
QY 454 -----GGCTTTTCATATAGTATACGGTTGATGGTCCATTAAACCTGTAACTGGGTC 507
Db 499 GCCATAGGATTTCTGATGCGGAACAGAGGAAGGTCTCTCAATCCCGTCAACGGTGTG 558
QY 508 GTTCGAAATTCGAGCTTTGACGAGTTTCAGGCGCGGTACCCAACTGATGATGCCACTGTG 567
Db 559 GTTCGAGGATAGTTCTTTCGCTGGCTCAGGGTCTGCTATCCCAAAATCAACGCTACCCCTG 618
QY 568 ATCG-----ATA 574
Db 619 ACCGGTAATTTCTCAACAACTGTCATTTCTCTAGTTTAGAGCTAAAGCTGACTAGATA 678
QY 575 CTACCAATCTTCGCGAGAGCGGCTTGGGAGATCTCTCAAGATTCCTTAGTGACTAC 634
Db 679 CCACCGAGCTCCCGGAAGGCACCTTGGGAAGTCTGCAAGGCTTCTCGGTGGTCTAC 738
QY 635 CTAGCTTGACTCTAGGTCAGTCTTAAGGACTTCAAGTCTATGAGCGAGAGCTATGGAG 694
Db 739 CTCAGTTGACAGCACTATCAAGTCCAAAGACTTTAATTTATGGAAGTGTAGGTTACGGAG 798
QY 695 GGCATATGGTCTGATCTTCAATTCATTTTACGAGCAGATGAGAGATTTGCCAAGC 754
Db 799 GACATACAGTCCCGATTTCTCAATCACTTTTACGAGCAGAACCAAAATTCGCAAGC 858
QY 755 GTAGTGTATATGGTTCAGCTTAATTTCAACTCTCTGGGAATTTAAGCGCATCATCG 814
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Db 979 TAGGCACCTTTCTACCTGATTTGGGGTGCAACAACCTTACGGCATCAAGCGGTGAGT 1038
QY 879 -----TGCAACGAGACCG 892
Db 1039 ACTGTCTTTTACGAATGACGACATACTTCAAGCTGAAACAGGTTTACGAGACAG 1098
QY 893 TCTACAACTCATGAGTTGGCAACCAATGCAATGGTTGGCAGGATTTGATTTCCA 952
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QY 1093 -----GACCCGACTCCGCCAAGTTATTAACAAATTTCTGGCAAGGACTCTGTGTAT 1145
Db 1399 GGAAGAGGACCAACACACCCCGAACCTCTTCGTCCTCTTCCAGCAAGACTTGGGTCTAT 1458
QY 1146 GGAAGC-TATCGCGCTGAAATCACTACACCCAGTCCCAATTAAGACCTCTACTACGCTT 1204
Db 1459 GAATGCTTTCTGGCGTGAAATCACTACCTCTTCCAAATAACGAAATTTACTATGCTT 1518
QY 1205 TCCAGCAACAGGCGACTTTGTCTGGCCCAACTTCATCGAAGACCTCGAGGAGATCTCTTG 1264
Db 1519 TCCAGCAACCGGTGATTTCTGTTGGCCCAACTTCATCGAGGATCTCGAGGAAATCTCTCA 1578
QY 1265 CTCTCCCGCTGCTGCTCTCTATGCGGAGCGCGATTAATCTGCAACTGTTCTG 1324
Db 1579 CCTACCCAGTCCGCTCAGTCTGATCTATGGCGACGAGACTACATCTGCAACTGTTCTG 1638
QY 1325 GGGTCAGCGCTTTCCCTCGCTCGAATCTCTCCAAAGCCGCCAGTTCCGAAGCGCAG 1384
Db 1639 GAGGCCAAGCGCTCTCCCTCGCCGTCAGAGTACCCGATTCAGAGGATTTCCAGGCGCGC 1698
QY 1385 GGTACACGCGCTGAAAGTCAACGCGCTCGAGTATGGGGAACCTCGCGAGTATGGTAAT 1444
Db 1699 GATACACGCTCTTCTTGTGATGCGTGGAGTACGAGAGACTCGAGAGTATGGCAAT 1758
QY 1445 TCTCTTCACTCGCTCTATGAGGCGCGCATGAAAGTCCATCTACAGCCCATCGCT 1504
Db 1759 TCTCTTCTCCGCTGTCTATGAGCGCGCCAGGTTCTCTTACTATCAGCCTGCTGCT 1818
QY 1505 CCCTCAATTTGTTAACCGGACTATCTTCGGTTGGATAT 1544
Db 1819 CGCTGAGCTTTTAAACCGCACTTTGTTGGTGGATAT 1858

RESULT 2
US-10-369-493-27042
; Sequence 27042, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27042
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27042

Query Match 5.5%; Score 91.6; DB 16; Length 1686;
Best Local Similarity 49.4%; Pred. No. 4.2e-19;
Matches 312; Conservative 0; Mismatches 299; Indels 21; Gaps 2;
QY 749 CCAACGGTAGTGTATGTTGTTGCTTCACTTCACTCTCTGGGAATTTAATTAACGCA 808

Db 842 CCAAGGCTGGCAGTAGTAAACCGGAAATATAAACTCACCTTGGCATCATGAACGGCT 901
QY TCATGAGAGGAGGATCCAGAGCCCTTACTACCTCGATTCCTGTGAACATACCTACG 868
Db 902 GCATCGAGCAGCTGCTCAAGGCTCCCGTACGTCGAGATGGCCATCAACACACGTCAG 961
QY GTATCAAGGCTGTCAACGAGACCGCTCTACAACTACATGAAGTTTGCCAAACCAATGGC-- 926
Db 962 GCATCAAGCTGATCGACCAAGCCAGCGCGGAGCCATCCTCTGGGCTTCAACGCCCTG 1021
QY 927 -AAATGGTTGGCAGATTTGATTTCCACTGCAACAGACAAACCGCACCCATTAAGTCG 985
Db 1022 ACAGGGGTGCAAGAGACCTGATCTCGCTTCCGCGCAAGCCCAAGCCGCTCTCGACCGC 1081
QY 986 ACTAGCCCTCTGCGCGAAGCCACCACTATGTCAGGGAATGTTGAGGGGCACTACT 1045
Db 1082 TGGACCAAGGTACCGACGAAACCGCTCAACCAAGGCTTGGCGCTACGCTCTACCTGCC 1141
QY 1046 ACGCCTTTGC-----TGGTCGTGGTGTCTATGATATTCGGCATCCAT 1087
Db 1142 AGCAGCTCCTCGGCTCGCTCGCCAGTGGCGCTAATGCCATAGCAATTGCGACATGG 1201
QY 1088 ATGATGACCGGACTCCGCGCAAGTTATTACAACTTTGCGCAAGAGCTCTCTCATGG 1147
Db 1202 GTCCCGATGCGTTTCCCGGATTTACCACCTACCTCGAGTATCTCAACTCGCGCGCGTGAAG 1261
QY 1148 ACGTATCGGCGTCAACATCAACTACACCTACACCCAGTCCATATGAGCTCTACTACGCTTCC 1207
Db 1262 AGCGATCGGCTCGTGGTCACTACACGAGATATTCGCGCGTAGTCTTACCAAGCCTTTT 1321
QY 1208 AGCAACAGCGGACTTTGTCTGCGCCCACTTTCATCGAAGACCTCGAGGAGATCCTTGCTC 1267
Db 1322 TCCAAACCGGGATAGGCTCGCGCGGCTGTATGCGCAAGCTAGCTTCGCTTCGAGC 1381
QY 1268 TCCCGTGGTGTCTCCCTCATCTATGCGGACGCGGATTAATCTGCAACTGGTTCGGCG 1327
Db 1382 GCGGCGTGGCATCGGCTCTGGTGTATGCGGACCGGATTAATCTGCAACTGGATGGCG 1441
QY 1328 GTACAGGCGGTTTCCCTCGCTCGGAACCTACTCC 1359
Db 1442 GCGAAGCGGTCTCTGGCTCTTCCGACGCC 1473

RESULT 3

US-09-993-192-1
; Sequence 1, Application US/09993192
; Publication No. US20020150983A1
; GENERAL INFORMATION:
; APPLICANT: Korea Research Institute of Bioscience and Biotechnology
; APPLICANT: Dong Kook Pharmaceutical Co.
; APPLICANT: Rhee, Sangki
; APPLICANT: Choi, Euisung
; APPLICANT: Kang, Hyunah
; APPLICANT: Sohn, Junghoon
; APPLICANT: Bae, Junghoon
; APPLICANT: Kim, Moowoong
; APPLICANT: Agaphonov, Michasel
; TITLE OF INVENTION: Hansenula polymorpha mutants and process for the preparation of
; TITLE OF INVENTION: recombinant proteins using the same
; FILE REFERENCE: 4220-116 US
; CURRENT APPLICATION NUMBER: US/09/993,192
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US/09/674,617A
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: PCT/KR00/00173
; PRIOR FILING DATE: 2000-03-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Hansenula polymorpha DLI
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: US/09/993,192
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US/09/674,617A
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: PCT/KR00/00173
; PRIOR FILING DATE: 2000-03-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Hansenula polymorpha DLI
; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: U67174
; DATABASE ENTRY DATE: 1996-08-17
; RELEVANT RESIDUES: (1)..(2218)
US-09-993-192-1

Query Match 4.2%; Score 70.6; DB 13; Length 2218;
Best Local Similarity 53.4%; Pred. No. 5.6e-12;
Matches 148; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 241 CATACCTTCTTCTGGTTCTTCGAAGCCAGACATAAACCCAGAAACTGCACCTTATCACATTG 300
Db 840 CATTTCTTCTATTTGATGTTTGAATCCAGAAATGACCCGGTCAACGACCTGTGATTCG 899
QY 301 TGGTTGAATGGTGGCCCTCGAAGCGATCTTTTGAATCGGTCTCTTCGAAGAGTTGGGCCCT 360
Db 900 TGGCTCAACGGTGGTTCAGGATGCTCTTCTTGAATGCTTTTGGAGCTCGGCTCT 959
QY 361 TGCCATGTCATTCGACTTTTGTGATGACTACATCAACCTCACTCGTGAAGAGGTCTCC 420
Db 960 GTTCTATCGTCCAGATCTCAAGCCATCAACCAACCCATATTCTGTGAATTCCAATGCC 1019
QY 421 AATTTACTATTCTCTGCCAGCCATTTGGGAGTCCGCTTTTCATATAGTATACGTTGAT 480
Db 1020 ACTGTGATTTTCTTGTACCGAGCTGTCAATGTTGATTTCTGTAATCTTCCAAGTCTGTT 1079
QY 481 GGGTCCATTAACCTCTTAATCTGGGCTCGTGAATAATT 517
Db 1080 TCTAACACGTCGCGAGCTGGTAAAGACGTCTATGCTT 1116

RESULT 4

US-10-206-619-1
; Sequence 1, Application US/10206619
; Publication No. US20030108908A1
; GENERAL INFORMATION:
; APPLICANT: Korea Research Institute of Bioscience and Biotechnology
; APPLICANT: Dong Kook Pharmaceutical Co.
; APPLICANT: Rhee, Sangki
; APPLICANT: Choi, Euisung
; APPLICANT: Kang, Hyunah
; APPLICANT: Sohn, Junghoon
; APPLICANT: Bae, Junghoon
; APPLICANT: Kim, Moowoong
; APPLICANT: Agaphonov, Michasel
; TITLE OF INVENTION: Hansenula polymorpha mutants and process for the preparation of
; TITLE OF INVENTION: recombinant proteins using the same
; FILE REFERENCE: 4220-116 US
; CURRENT APPLICATION NUMBER: US/10/206,619
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US/09/674,617
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: PCT/KR00/00173
; PRIOR FILING DATE: 2000-03-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Hansenula polymorpha DLI
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U67174
; DATABASE ENTRY DATE: 1996-08-17
; RELEVANT RESIDUES: (1)..(2218)
US-10-206-619-1

Query Match 4.2%; Score 70.6; DB 15; Length 2218;
Best Local Similarity 53.4%; Pred. No. 5.6e-12;
Matches 148; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 241 CATACCTTCTTCTGGTTCTTCGAAGCCAGACATAAACCCAGAAACTGCACCTTATCACATTG 300
Db 840 CATTTCTTCTATTTGATGTTTGAATCCAGAAATGACCCGGTCAACGACCTGTGATTCG 899

Qy	314	GCCCTGGAAGCGATCTTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCCCATGTCAATT	373
Db	187	GCCTTGGTGTCTCTCTCACTGGACTCTTCATGGAGCTTGGGCCACGAGTATTGATG	246
Qy	374	CGACTTTTGATGACTACATCAATCAACCCCTCACTCGTGGAAACGAGGCTTCCAAATTACTATTGCC	433
Db	247	AGAAATCAACGCGGTTTATAACCCGTTATGCTGTGGAACCTCCAACGCTTCGGTTATCTTCT	306
Qy	434	TGTCCACGCCATTGGGAGTCGGCTTTTCATATAGTGTATACGGTTGATGGTCCCATTAACC	493
Db	307	TGGACCAACCGCTCAACGTTGGCTACTCTTACAGCGGCAGTACTGTACGGACACTGTGG	366
Qy	494	CTGTAACTGGGGTGGT	509
Db	367	CTGCTGGAAGGACGT	382

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RESULT 8
US-10-369-493-25156
; Sequence 25156, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 25156
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-25156

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Query Match	3.7%;	Score 61.8;	DB 16;	Length 1527;
Best Local Similarity	51.6%;	Pred. No. 4e-09;		
Matches 141;	Conservative 0;	Mismatches 132;	Indels 0;	Gaps 0;
QY	199	GTCAATCTCTCTGGATATGTCGACACCTCTCCGAGTCCCAATACCTTCTTCTGTGTC	258	
Db	271	GTAAAACAATGGTGGGTTACATGGACTAAGGATTCCAAACACTTTTTTACTGGTTT	330	
QY	259	TTCCGAGCCAGACATAAACCCAGAAATGCGACCTTATCACATTTGGTTGAATGGTGGCCCT	318	
Db	331	TTTGAAGTAGGACGATCTCTGTACGACCCAAATTATCTTTGGTTAAATGGTGGACCT	390	
QY	319	GGAAGCGATTCTTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCCATGCAATCGACT	378	
Db	391	GGTTGTCTCTCGTTTACTGGTTGCTATTTGAATAGGCCCTTCATCAATGGGCGCGAT	450	
QY	379	TTTGATGACTACATCAACCCCTCACTCGTGGAAAGAGGTCTTCCAATTACTATTCTCTGCC	438	
Db	451	ATGAACCAACATCCCAATCCCTATTCTTGAATATAACGCTTCAATGATCTTCTTAGAA	510	
QY	439	CAGCCATTGGGAGTCGGCTTTTCATATAGTAT	471	
Db	511	CAGCCACTCGGAGTCGGCTTTTCTCATATGGTAT	543	

RESULT 9
US-09-736-457-319
; Sequence 319. Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

```

? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Lodes, Michael A.
? APPLICANT: Fanger, Gary
? APPLICANT: Vedvick, Tom
? APPLICANT: Carter, Darrick
? APPLICANT: Retter, Marc
? APPLICANT: Mannion, Jane
? APPLICANT: Fan, Liqun
? APPLICANT: Wang, Aijun
? TITLE OF INVENTION: COMPOSITIONS AND METHODS
? TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.479C15
? CURRENT APPLICATION NUMBER: US/09/736,457
? CURRENT FILING DATE: 2000-12-13
? NUMBER OF SEQ ID NOS: 1864
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 319
? LENGTH: 1814
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-736-457-319

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Query Match	3.4%	Score 56.4	DB 9	Length 1814
Best Local Similarity	52.5%	Pred. No. 2.9e-07		
Matches 148	Conservative 0	Mismatches 131	Indels 3	Gaps 1
QY	193	CCGGGTGTCAAATCCTACTCTCGATATGTCGACACCTCTCCCGAGTCCCATACCTTCCTC	252	
Db	139	CCGTCTTTCCGCCAGTACTCTCGGTACTCTCAAAAGCTCCGGCTCCAAAGCACCTCCACATAC	198	
QY	253	TGCTTCTTCGAAGCCAGACATAACCCAGAAACTGCACCTATCATCTTGTGTTGAATGGT	312	
Db	199	TGTTTTGTGGAGTCCCAAGAGATCCCGAAACAGCCCTTGTGGTCTTTGGCTCAATGGG	258	
QY	313	GGCCCTCGGAAGCGATCTTTTGATCGGTCTCTTCGAAGAGTTGGGCCCTTGCATGTCAAT	372	
Db	259	GGTCCCGGCTGCAGCTCACTAGATGGGTCTCTACAGAGCATGGCCCTTCTCTGGTCCAG	318	
QY	373	TCGACTTTTGTAGTACT---ACATCAACCCCTCACTCGTGGAAACGAGGTCTCCAAATTACTA	429	
Db	319	CCAGATGGTGTACCCCTGGAGTACACCCCTATTCTTGGAAATCTGATTTGCCAATGTGTTA	378	
QY	430	TTCCCTGCCAGCANTGGGAGTCGGCTTTTCATATAGTGAT	471	
Db	379	TACCTGGAGTCCCGAGCTGGGGTGGGTTCTCTACTCCCGAT	420	

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RECORD 10
US-09-902-941-319
; Sequence 319, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/302,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 1814
; TYPE: DNA

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; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-017-319

Query Match
Best Local Similarity 3.4%; Score 56.4; DB 13; Length 1814;
Matches 148; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

QY 193 CCGGTGTCAAATCTTCTGATATGTCGACACTCTCCGAGTCCCATACCTTCTTC 252
Db 139 CCGTCTTTCCGCGAGTACTCCGGCTACCTCAAAAGCTCCGGCTCCAGACCTCCACTAC 198

QY 253 TGGTCTTCGAGCCAGACATACCCAGAACTGCACCTATCACATTTGGTGTGAATGGT 312
Db 199 TGGTTTGGAGTCCGAGAGGATCCGAGAACAGCCCTGTGGTCTTTGGCTCAATGGG 258

QY 313 GGCCCTGGAAGCGAATCTTTGATCGTCTCTTCGAAAGATTGGGCCCTTGCATGCAAT 372
Db 259 GGTCGCCGCTGAGCTACTAGATGGGCTCTCCAGAGCATGGGCCCTTCTCTGGTCCAG 318

QY 373 TCGACTTTTGTAGTACT---ACATCAACCTCACTCGTGGAGCGAGTCTCCAAATTTACTA 429
Db 319 CCAGATGGTGTACCCCTGGAGTACCAACCCCTATTCTTGGAAATCTGATTGCCAATGTGTTA 378

QY 430 TTCTGTCTCCAGCCATTCGGGTGAGTCCGCTTTTCATATAGTAT 471
Db 379 TACCTGGAGTCCCGAGCTGGGGTGGGCTTCTCTACTCCGAT 420
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RESULT 14

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US-10-017-754-319
; Sequence 319 Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-754-319

Query Match
Best Local Similarity 3.4%; Score 56.4; DB 15; Length 1814;
Matches 148; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

QY 193 CCGGTGTCAAATCTTCTGATATGTCGACACTCTCCGAGTCCCATACCTTCTTC 252
Db 139 CCGTCTTTCCGCGAGTACTCCGGCTACCTCAAAAGCTCCGGCTCCAGACCTCCACTAC 198

QY 253 TGGTCTTCGAGCCAGACATACCCAGAACTGCACCTATCACATTTGGTGTGAATGGT 312
Db 199 TGGTTTGGAGTCCGAGAGGATCCGAGAACAGCCCTGTGGTCTTTGGCTCAATGGG 258
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QY 313 GGCCCTGGAAGCGAATCTTTGATCGTCTCTTCGAAAGATTGGGCCCTTGCATGCAAT 372
Db 259 GGTCCCGGCTGCAGCTCACTAGATGGGCTCTCCAGAGCATGGGCCCTTCTCTGGTCCAG 318

QY 373 TCGACTTTTGTAGTACT---ACATCAACCTCACTCGTGGAGCGAGTCTCCAAATTTACTA 429
Db 319 CCAGATGGTGTACCCCTGGAGTACCAACCCCTATTCTTGGAAATCTGATTGCCAATGTGTTA 378

QY 430 TTCTGTCTCCAGCCATTCGGGTGAGTCCGCTTTTCATATAGTAT 471
Db 379 TACCTGGAGTCCCGAGCTGGGGTGGGCTTCTCTACTCCGAT 420

RESULT 15
US-10-113-872-319
; Sequence 319 Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-113-872-319
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Query Match
Best Local Similarity 3.4%; Score 56.4; DB 15; Length 1814;
Matches 148; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

QY 193 CCGGTGTCAAATCTTCTGATATGTCGACACTCTCCGAGTCCCATACCTTCTTC 252
Db 139 CCGTCTTTCCGCGAGTACTCCGGCTACCTCAAAAGCTCCGGCTCCAGACCTCCACTAC 198

QY 253 TGGTCTTCGAGCCAGACATACCCAGAACTGCACCTATCACATTTGGTGTGAATGGT 312
Db 199 TGGTTTGGAGTCCGAGAGGATCCGAGAACAGCCCTGTGGTCTTTGGCTCAATGGG 258

QY 313 GGCCCTGGAAGCGAATCTTTGATCGTCTCTTCGAAAGATTGGGCCCTTGCATGCAAT 372
Db 259 GGTCCCGGCTGCAGCTCACTAGATGGGCTCTCCAGAGCATGGGCCCTTCTCTGGTCCAG 318

QY 373 TCGACTTTTGTAGTACT---ACATCAACCTCACTCGTGGAGCGAGTCTCCAAATTTACTA 429
Db 319 CCAGATGGTGTACCCCTGGAGTACCAACCCCTATTCTTGGAAATCTGATTGCCAATGTGTTA 378

QY 430 TTCTGTCTCCAGCCATTCGGGTGAGTCCGCTTTTCATATAGTAT 471
Db 379 TACCTGGAGTCCCGAGCTGGGGTGGGCTTCTCTACTCCGAT 420
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Search completed: July 29, 2004, 13:35:46
Job time : 794 secs

16	455	15.3	500	16	US-10-437-963-156046	Sequence 156046,
17	417.5	14.0	2105	15	US-10-369-493-7002	Sequence 7002, App
18	417.5	14.0	2105	15	US-10-369-493-7003	Sequence 7003, App
19	417.5	14.0	2105	15	US-10-369-493-7004	Sequence 7004, App
20	385	12.9	474	16	US-10-437-963-159639	Sequence 159639,
21	382	12.8	526	12	US-10-425-114-65212	Sequence 65212, A
22	381	12.8	524	16	US-10-437-963-152087	Sequence 152087,
23	375.5	12.6	358	12	US-10-425-114-40609	Sequence 40609, A
24	375.5	12.6	500	16	US-10-437-963-200236	Sequence 200236,
25	372	12.5	467	12	US-10-424-599-169015	Sequence 169015,
26	368	12.4	489	12	US-10-425-114-64560	Sequence 64560, A
27	364	12.2	461	12	US-10-425-114-56187	Sequence 56187, A
28	361	12.1	476	13	US-10-084-018-3	Sequence 3, Appli
29	360	12.1	493	12	US-10-424-599-282093	Sequence 282093,
30	359	12.1	476	9	US-09-909-320-164	Sequence 164, App
31	359	12.1	476	9	US-09-909-088B-164	Sequence 164, App
32	359	12.1	476	9	US-09-905-291A-164	Sequence 164, App
33	359	12.1	476	9	US-09-902-853-164	Sequence 164, App
34	359	12.1	476	9	US-09-907-824-164	Sequence 164, App
35	359	12.1	476	9	US-09-907-841-164	Sequence 164, App
36	359	12.1	476	10	US-09-904-011-164	Sequence 164, App
37	359	12.1	476	10	US-09-906-742-164	Sequence 164, App
38	359	12.1	476	10	US-09-906-838-164	Sequence 164, App
39	359	12.1	476	10	US-09-907-613-164	Sequence 164, App
40	359	12.1	476	10	US-09-907-5942-164	Sequence 40, Appl
41	359	12.1	476	10	US-09-796-753-40	Sequence 164, App
42	359	12.1	476	10	US-09-904-859-164	Sequence 164, App
43	359	12.1	476	10	US-09-909-204-164	Sequence 164, App
44	359	12.1	476	10	US-09-904-820-164	Sequence 164, App
45	359	12.1	476	10	US-09-904-786-164	Sequence 164, App

RESULT 1

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US-10-369-493-12894
; Sequence 12894, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTIC
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12894
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Aspergillus nidulans

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26 SVGRQLPKNPFGVKLTLLANNVIRYKEPGAEGVCETTPGVKSYSGYVDTSPESTFPW 85
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
7 SENRQLPADATGVKKFPTNGVIRYKEPCKEVCCTTPGVNSYSYGYVDLSPESTFFY 66
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
86 FFEARHPETAPITLWLNGPGSGLGLPF-----ELGFCVHNST 126
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1722	57.8	617	15	US-10-369-493-12894		Sequence 12894, A
2	812.5	27.3	562	15	US-10-369-493-3355		Sequence 3355, Ap
3	636	21.3	508	15	US-10-369-493-1469		Sequence 1469, Ap
4	559.5	18.8	429	15	US-10-369-493-13233		Sequence 13233, A
5	550	18.5	539	15	US-10-369-493-3911		Sequence 3911, Ap
6	527.5	17.7	532	15	US-10-369-493-1926		Sequence 1926, Ap
7	517.5	17.4	421	9	US-09-420-7854-4		Sequence 4, Appli
8	517.5	17.4	421	9	US-09-901-252-15		Sequence 15, Appl
9	473.5	15.9	500	12	US-10-425-114-48698		Sequence 48698, A
10	473	15.9	525	12	US-10-425-114-44602		Sequence 44602, A
11	468	15.7	525	16	US-10-437-963-155055		Sequence 155055, S
12	463	15.5	462	12	US-10-424-599-202253		Sequence 202253, S
13	462.5	15.5	508	15	US-10-382-2398-2		Sequence 2, Appli
14	458.5	15.4	484	12	US-10-424-599-214407		Sequence 214407, S
15	455	15.3	499	12	US-10-424-599-172991		Sequence 172991, S

Db 67 FFEARHDPANAPITLWMLNGPGSDSLGLFEGLYCLTGLQEVVDVLMFLGELPCALSEN 126

QY 127 FDDYINPHSNVEVSNLFLSLOPLGVG-----FSYSDTVGDSINPVTGVVENSFF 175

Db 127 LTTVYNPYSNVEVSNLFLSLOPLGVGKMLCLVNSCSFSGLGHRIFVCGN--RGRVAQSRH 184

QY 176 AGVQG-----RYPTID-----ATLIDTNNLAAEAWEILOQFELS 209

Db 185 RCRGXFRWRPGLSQRVYDRXFLQORALSXFRAKAVLDTTTELAAKATWEVVOGFLG 244

QY 210 GLPSLDRVQSKDFSLWTESGGHYGPAFNHFFVEQNERIANGSVNGVOLFNSLIGLNG 269

Db 245 GLPOLDSITKDFNLWTESGGHYGPAFNHFFVEQNERIANGSVNGVOLFNSLIGLNG 304

QY 270 IIDRAIQ-----APYYP-----EFAVNNTY-----GIXAVN 295

Db 305 IIDREGIQRDRAAQYLSDXKLTFLPXVCGAQLRHSREYCLFSKWTXTLTSXKQVN 364

QY 296 ETVNYMKFANOMPNGCODLISTCKQTNRTALADYALCAEATNMCRDNVEGYY----- 349

Db 365 ETVNYMKFANEMNGCQDIALCKATNRSSFDYALCSEATNMCRDNV--GTIFYLRLWE 423

QY 350 ----AFAGRV-----YDIRHPYD-----DTPPSYXNKFLAK 378

Db 424 SNQLIIFHRGTPTTGYEQLEAYMDIRHPHNVSRXSRSFSILTKEKDTPTPNLFPVFLQ 483

QY 379 DSVMDAIGVNTYOSNDVYVAFQOTGDFVWPNFIEDLEILALPVRVSLIYGDADYIC 438

Db 484 DWMNASVNVNNTSSNEIYVAFQOTGDFVWPNFIEDLEILALPVRVSLIYGDADYIC 543

QY 439 NWFQGOAVSLAANYSOAQRAGTYPLKVNVEYGETREYGNFSTRVYAGHEVPYYQ 498

Db 544 NWFQGOAVSLAVKYPHSGKQFAAGYTPLLVDGVGEYGETREYGNFSTRVYAGHEVPYYQ 603

QY 499 PIASIQLENRTIFG 512

Db 604 PAASIQLENRTIFG 617

RESULT 2

US-10-369-493-3355

; Sequence 3355, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 3355

; LENGTH: 562

; TYPE: PRT

; ORGANISM: Neurospora crassa

US-10-369-493-3355

Query Match 27.3%; Score 812.5; DB 15; Length 562;

Best Local Similarity 36.0%; Pred. No. 1.9e-67;

Matches 198; Conservative 83; Mismatches 182; Indels 87; Gaps 19;

QY 33 PKNPTGVKTLTAN--NVTRYKEPAGEGVCEIT--FGVKSYSGYVDTSPS--SHTFEPWF 87

Db 28 PYQAVGLKTVTSPSNPIKISKEP--KDVCTTAFRQKQYTGWTVVPGVYTHLFPWFV 85

QY 88 EARNHPETAPITLWMLNGPGSDSLGLFELGPGCHV-----NSTPDDYINPHSNVEVSNLL 143

Db 86 GARE--PTSALTWMLNGPGSSSMFGLFAENGPCQVVEKGASRLETAAREWGMDRASNML 143

QY 144 FLSQPLGVGSYSYSDTVGDSINPVTGVVE-----NSSFA--GVQGRYPTID 186

Db 144 FVDQPNHVGFSYDPTPTNGSLDLTITGMVSPPTMQPLPDNLPPSLFLNGTFTSSNNIQ----- 196

QY 187 ATLIDTNNLAAEAWEILOQFELGSLPS--LDSRVQSKDFSLWTESYGGHYGPAFNHFFVEQ 245

Db 197 -NTANTTQNDAMAVYHLLQGLSTFTFPYVDPKHSPLGVNLFSTESYGGHYGPFVADTWQKE 255

QY 246 NERIANGSV-----NGVQ-----LNFNSLGIINGIIDEALQAPYYPFEFA 284

Db 256 NDKLSKRAMPLSRQDDANNIQRPPKAGSSNREIKLTSLGIMNGCDDLLVQGSRYVEMA 315

QY 285 VNNYTGKAVNTEVYNYMKFANOMPNGCODLISTCKQ-----TNRTALADYAL 332

Db 316 INNTYGIKLIDQATADAITSGFNAPDTGCKDLIILACQAQALDPLDQGTDTV---NQV 372

QY 333 CAEATNMCRDNVEGYYAFAGRVYDIRHPYDPTTPSYXNKFLAKDSVMDAIGVNTY 392

Db 373 CAYASLTCQ--QLLSGVLA--SGANAYDIAHMGEPDAPPDYHLYEYLSNRRVQEAIGSVVNYT 430

QY 393 QSNNDVYVAFQOTGDFVWPNFIEDLEILALPVRVSLIYGDADYICNWFQGOAVSLA--- 449

Db 431 DISPVYQAFQOTGDRARGGLIAKLASLLQRGVIRGLVYGRDYICNMWGGEAVSLALAD 490

QY 450 -----ANYSQAQFRSAGTYPLKVNVEY--GETREYGNFSTRVYAGHEVPYYQPIAS 502

Db 491 AMEDLPKSPYTPKPOAGYENIQTNREVGVGVVRFQGNLSFSLYQSGHFVPAQOPETA 550

QY 503 LQLENRTIFG 512

Db 551 FRVFERIIGG 560

RESULT 3

US-10-369-493-1469

; Sequence 1469, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 1469

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-1469

Query Match 21.3%; Score 636; DB 15; Length 508;

Best Local Similarity 32.6%; Pred. No. 7.6e-51;

Matches 167; Conservative 70; Mismatches 197; Indels 78; Gaps 14;

QY 19 LPQSTPASVGRROL----PKNPTGVKTLTANNTVTRYKEPAGEGVCEITTPGVKSYSGYV 74

Db 43 LPQNTQOTLUKLDKLNHDDPLFTFTSSVDTLSLRRTVDPKSLGI---DTVKQSGYM 98

QY 75 DTSPESHTFWFPEARNPETAITLWMLNGPGSDSLGLFELGPGCHVNSTPDDYINPH 134

Db 99 DYKDSKHFFWFPEARNPETAITLWMLNGPGSDSLGLFELGPGCHVNSTPDDYINPH 158

QY 135 SNNEVSNLLPLSQPLGVGSYSDTVGDSINPVTGVVENSFFAGVQGRYPTIDATLIDTIN 194

Db 159 SWNNASMIFFLEQLGVGFSGYD-----EKVSSTK 188
 QY 195 LAEEAAWIILOFLSGLSDSRVQSKDFSLWTSYSGHYGPAPFNHFYEQN-BRIANGS 253
 Db 189 LAGRDAYIFLELFFAFPHL-----RSNDFHAGESYAGHYTPQIAHEIVVKNPER-----239
 QY 254 VNGVQLNFSLGIINGIIDEAIOAPYPPEFAV-NTYGIKAVNTVYNYMKFANQMPNGC 312
 Db 240 ----TFNLTSVMIGNGITDPLIQADYBPMACGKGYPVLSSECEKWSKAAGR-----290
 QY 313 QDLISTCKQNTALADYAL--CAEATNMCRDNVEGYPYAFAGRGVYDIRHPYDDP-----366
 Db 291 -----CARLNKLVCASKSSLPICVATAYCDASALLEPYIN-TGLNVYDIRGPCEDNSTG 343
 QY 367 ---TPPSYNNKFLAKDSVMDAIGVNI-NTYQSNNDVYVAFQOTGDFVWPNFIEDLEETLA 422
 Db 344 MCYTGLRVQVMNPFVEQETLSGDVHNSGCDNDVFTGFLFTGDSKP-FQQYIAELLN 402
 QY 423 LPVRVSLYGDADYICNWFQGOAVSLAANYSQAAQFRSAGYTP--LKVNGVEYGETREYG 480
 Db 403 HNIPLVLIYAGDKYICNWLGNHWSNELEWINKRYQRMLRPWVSKETGELGOVKNYG 462
 QY 481 NFSFTRVVEAGHEVPYQYPTASLOLFNRTIPG 512
 Db 463 PFTFLRIYDAGHWPYDQPEASLEWNSWISG 494

RESULT 4

US-10-369-493-13233
 ; Sequence 13233, Application US/10369493
 ; Publication No. US20030233675A1

GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 13233

; LENGTH: 429
 ; TYPE: PRT

; ORGANISM: Aspergillus nidulans
 ; FEATURE:

; NAME/KEY: unsure
 ; LOCATION: (1)..(429)

; OTHER INFORMATION: unsure at all xaa locations
 US-10-369-493-13233

Query Match 18.8%; Score 559.5; DB 15; Length 429;
 Best Local Similarity 30.7%; Pred. No. 9.9e-44;
 Matches 149; Conservative 71; Mismatches 169; Indels 97; Gaps 19;

QY 65 PGVKSYSYGVDTSP-ESHTFF-----WFFEARHNPETAPITLWNGG 105

Db 4 PDVKQVTGLDNDENDKHFLYLVXVDIIVVIGRVYXRAEGFESRNDKNDPWLWNGG 63

QY 106 PGSDSLIGLFEELGPGCHVNSTDDYINPHSWNEVSNLLFLSPLGVSFYSYTDVDSINP 165

Db 64 PGCSLSLTLGFMELGPSIDENIKPTVNPYAMNSASVIFLDQPVNVGYSYS-----114

QY 166 VTGVVNSSFAGVQGRYPTIDATLDTTNLAEEAAWEIILQGLSLGPSLDSRVQSKDFSL 225

Db 115 -----GSTVSDTV-AAGKDVVALLTLFFKQFP-----EYAQDQFHI 149

QY 226 WTESYGGHYGPAFFNHFYQNERIANGSVNGVQLNFSNGIINGIIDEAIOAPYPPEFAV 285

Db 150 AGESYAGHYIIPVFTSEILSHOKR-----NINLKSVLINGELTDLGTQVEYYRPMAC 200
 QY 286 NNTYGIKAVNETVYNYMKFANQMPNG-----CODLISTCKQNTALADYALCAEATNMCRD 342
 Db 201 GEG-GYPAVLDE-----SSCRSDNALGRCSMIESCYNSESA-----WVCVPASIYCNN 249
 QY 343 NVEGYPYAFAGRGVYDIRHPYDDPT-----PPSYNNKFLAKDSVMDAIGVNI-NTYQSN 396
 Db 250 ALLAPYQR-TQONYDVRGKCEDSNLCYKMGVYSEYINKPEVRAAVGAEDVDGSCNF 308
 QY 397 DVYVAFQOTGDFVWP--NFIEDLEIILALPVRVSLIV-GDADYICNWFQGOAVSLAANY 453
 Db 309 DINENFLFHGDWMPYHRLVPGILE--QIPV--LIVAGDADFICNMLGNKAWTEALEWP 363
 QY 454 QAAQFRSAGYTPPKV-----NGVEYGETREYGNFSFTRVVEAGHEVPYQYPTASLOLFN 508
 Db 364 GHKEFAAAPMEDLKIVDNEHTGKIGIKTHGNFTFMRLYGGGHVWPMQDPEASLEFENR 423
 QY 509 TIFG-W 513
 Db 424 WLGGEW 429

RESULT 5

US-10-369-493-3911

; Sequence 3911, Application US/10369493
 ; Publication No. US20030233675A1

GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 3911

; LENGTH: 539
 ; TYPE: PRT

; ORGANISM: Neurospora crassa
 ; FEATURE:

; NAME/KEY: unsure
 ; LOCATION: (1)..(539)

; OTHER INFORMATION: unsure at all xaa locations
 US-10-369-493-3911

Query Match 18.5%; Score 550; DB 15; Length 539;
 Best Local Similarity 30.7%; Pred. No. 1.1e-42;
 Matches 154; Conservative 66; Mismatches 187; Indels 94; Gaps 18;

QY 47 NVTIRYKEPGAGVCETTPGVKSYSYGVDTSP-ESHTFF-----84

Db 99 NLRVKSVDPFSLGVDK-----VKQSYGLDDEENDKHFLYLVXVNHARMYLVSNKHGADSDC 154

QY 85 -WFFEARHNPETAPITLWNGGPGSDSLIGLFEELGPGCHVNSTDDYINPHSWNEVSNLL 143

Db 155 PGFFESRNDKNDPVLWNGGPGSCSLTGLFELGPSIDKKLRVSWNEVANNASVI 214

QY 144 FLQSPLGVGFYSYDVTGDSINPVTGVWENSSFAGVQGRYPTIDATLDTTNLAEEAAWEI 203

Db 215 FLDQPVNVGYSYS-----GNAVSTVAAGKDVVAL 244

QY 204 LQGLSLGPSLDSRVQSKDFSLWTSYGGHYGPAFFNHFYQNERIANGSVNGVQLNFS 263

Db 245 LTLFFHQFP-----EYAQDQFHIAGESYAGHYIIPVFASEILSHKDR-----NINLKS 291

QY 264 LGILINGIIDEAIOAPYPPEFAVNNTYGIKAVNETVYNYMKFANQMPNGCODLISTCKQTN 323

Db 292 VLIQNGLTDLPTQYEHYRPMACGEGGYPVLSBSECRSMD--NALPR-COSLIRNCVES- 347

Qy 324 RTALADYALCAEATNMCRDNVEGYPYAFAGRGVYDIRHPYDDTPPSY-----YNKFLAK 378

Db 348 -----GSWSCVPAIYCNQGFIPYQYR-TGQNVYDIRKCEDDSNLCYSALGMSIDYLNQ 402

Qy 379 DSVMDAIGVNI-NYTSQNNDDVYAFQOTGDFVWPNFTDLEEL-ALPVRVSLIY-CDAD 435

Db 403 KDVMALGVEGYESCNDINRNFQGDWQBP-FHRLVPGILKEIFV---LIYAGDAD 458

Qy 436 YICWFGGQAVSLAANYSQAAQFSAAGTYPLKNGV--EYGETREYGNESFTRVYAGHE 493

Db 459 FICWNLGNKAWSEALEVPGKNGFNKALEDLSLPKADKEYGKVKSSGNFTFMQIYQAGHM 518

Qy 494 VPIYQPIASLQLENRTIFG-W 513

Db 519 VPMDQPENSLDFLNRWLGGEW 539

RESULT 6

US-10-369-493-1926

; Sequence 1926, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 1926

; LENGTH: 532

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-1926

Query Match 17.7%; Score 527.5; DB 15; Length 532;

Best Local Similarity 29.1%; Pred. No. 1.5e-40;

Matches 149; Conservative 71; Mismatches 195; Indels 97; Gaps 19;

Qy 33 PKNPTGVKT-----LTTANNVTIRY-----KEPGAAGVCETTPGVKSYSGVDTSP- 79

Db 82 PKFPEAIKTKQWDFVVKNDATENYQIRVNKIKDPKILGI:---DPNVQTYGLDVEDED 138

Qy 80 SHTFWFFFEARHNPETAPITLWNGGSDSLGLFEELGCHVNSTFDDYINPHSWNEV 139

Db 139 KHFFFWTFESRNDPAKDPVILWNGGPGSSLTGLFELGPGSSIGPDLKPIGNPYSWNSN 198

Qy 140 SNLLFUSQLGVGFSYSDTVGSDINPVTGVNSFAGVQGRYPTIDATLITDNLAAEA 199

Db 199 ATVIFLDQPNVGVGFSY-----GSSG-----VSNVVAAGKD 229

Qy 200 AMEILQGLSLPSLDSRVQSDPSLWTSYGGHYGPAFNFHYEQNERIANGSVNGVQL 259

Db 230 VYNFLELFFDQFPEYVNGQ--DFHTAGESYAGHYLPVFASELSHKOR----- 276

Qy 260 NFNSLGI--NGHIDEAIQAPYYPEFA-----VNNTYGIKAVNETVYVYMKFANQMP 309

Db 277 NFNLTSVLINGLTDPLTOYNYEPMACGEGPSPVLPSECSAMEDSL----- 325

Qy 310 NGQDILSTCKQNTALADYALCAEATNMCRDNVEGYPYAFAGRGVYDIRHPYDD--- 365

Db 326 ERLGLIESCYDSQ-----SWMSCVPATIIYCNNAQIAPYOR-TGRNVYDIRKCEGNNLC 379

Qy 366 -PTPPSYNKLAKDSYMDAIGNVINYTQS--NNDVYAFQOTGDFVWPNFTDLEELAL 423

Db 380 YPTLQD-IDDYLNQDYVKEAVGAEDVHYESCNDINRNFACGMMKP-YHTAVTDLLNQ 437

Qy 424 PVRVSLIYGADYICWFGGQAVSLAANYSQAAQFSAAGTYPLKNGVVEGETREYG 480

Db 438 DLPILVYAGDKDFICWNLGNKAWTDVLPWKYDSEFASQKVRNWTASITDEVA-GEVKS 496

Qy 481 NFESFTRVYAGHEVPPYQPIASLQLENRTIFG 512

Db 497 HFTYLRVFGGHMVFPDVPENALSMVNEWIHG 528

RESULT 7

US-09-420-785A-4

; Sequence 4, Application US/09420785A

; Patent No. US2001001023A1

; GENERAL INFORMATION:

; APPLICANT: MORTENSEN, UFFE

; APPLICANT: OLESEN, KJELD

; APPLICANT: STENNICKKE, HENNING

; APPLICANT: SORENSSEN, STEEN B.

; APPLICANT: BREDDAM, KLAUS

; TITLE OF INVENTION: MODIFIED CARBOXYPEPTIDASE

; FILE REFERENCE: 089187/0109

; CURRENT APPLICATION NUMBER: US/09/420,785A

; CURRENT FILING DATE: 1999-10-19

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 421

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-09-420-785A-4

Query Match 17.4%; Score 517.5; DB 9; Length 421;

Best Local Similarity 29.5%; Pred. No. 8.9e-40;

Matches 142; Conservative 70; Mismatches 185; Indels 85; Gaps 17;

Qy 51 RYKPGAAGVCETTPGVKSYSGVDTSP-ESHTFEFFFEARHNPETAPITLWNGGPGSD 109

Db 1 KIKDPKILGI---DPNVQTYGLDVEDEDKHFFFTFESRNDPAKDPVILWNGGPGS 57

Qy 110 SLIGLFEELGCHVNSTFDDYINPHSWNEVSNLLFUSQLGVGFSYSDTVGSDINPVTG 169

Db 58 SLTGLFELGPGSSIGPDLKPIGNPYSWNSNATVIFLDQPNVGVGFSY----- 104

Qy 170 VENSFAGVQGRYPTIDATLITDNLAAEAWEILQGLSLGSLDSRVQSDKDFSLWTS 229

Db 105 -----GSSG-----VENTVAAGKDVNFLELFFDQFPEYVNGQ--DFHTAGES 146

Qy 230 YGGHYGPAFNFHYEQNERIANGSVNGVQLNFNSLGI--NGHIDEAIQAPYYPEFA--- 284

Db 147 YAGHYLPVFASELSHKOR-----NENLTSVLINGLTDPLTOYNYEPMACGE 195

Qy 285 -----VNNTYGIKAVNETVYVYMKFANQMPNCGQDILSTCKQNTALADYALCAEATNM 339

Db 196 GGEPSVLPSECSAMEDSL-----ERCLGLIESCYDSQ-----SWMSCVPATIIY 239

Qy 340 CRDNVEGYPYAFAGRGVYDIRHPYDD-----PTPPSYNKLAKDSYMDAIGNVINYTQS 394

Db 240 CNNAQIAPYOR-TGRNVYDIRKCEGNNLCYPTLQD-IDDYLNQDYVKEAVGAEDVHYES 297

Qy 395 -NNDVYAFQOTGDFVWPNFTDLEELALPVRVSLIYGADYICWFGGQAVSLAANY 453

Db 298 CNFDINRNFACGMMKP-YHTAVTDLLNQDLPILVYAGDKDFICWNLGNKAWTDVLPWK 356

Qy 454 QAAQFSAAGTYPLKNGVVEGETREYGNESFTRVYAGHEVPPYQPIASLQLENRTI 510

Db 357 YDEEFASQKVRNWTASITDEVA-GEVKSHTYHFTYLRVFGGHMVFPDVPENALSMVNEWI 415

Qy 511 FG 512

Db 416 HG 417

```

RESULT 8
; US-09-901-252-15
; Sequence 15, Application US/09901252
; Patent No. US20020026658A1
; GENERAL INFORMATION:
; APPLICANT: Chapple, Clint
; TITLE OF INVENTION: Genes Encoding Sinapoylglucose:Malate Sinapoyltransferase and Met
; TITLE OF INVENTION: Use
; FILE REFERENCE: N1422-004
; CURRENT APPLICATION NUMBER: US/09/901,252
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216593
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Saccharomyces
; US-09-901-252-15

```

Query Match		17.4%	Score 517.5;	DB 9;	Length 421;
Best local similarity		29.5%;	Pred. No. 8.9e+40;		
Matches 142;	Conservative	70;	Mismatches 185;	Indels	Gaps 17;
QY	51	RYPEKGAEGVCETTPGVKSISGVYDTSPE-SHTFFWFPEARHNPETAPITLWLNGGPGSD	109		
Db		: : :	: : :	: : :	: : :
1	KIKDKPKILGI--DPNVQTGTGLDVDEDEOKHFFFWTFESRNDPAKDPVILWLNGGFGCS	57			
QY	110	SLTGLFEELGPCHVNSTFDDYINPHSNVEYSNLLFLSQPLVGVSYSYDVTVDGSIINPTGV	169		
Db					
58	SLTGLFEELGPSSIGDLKPIGNPYSWNSATVIFLDQPNVGVFSYS-----	104			
QY	170	VENSSFAGVQGRYPTIDATLIDTNIAAEAAWEILOGLFLSGLSLDSRVQSKDFSLWTES	229		
Db		-----GSSG-----	--VSNVAAGKDVNYLELFDFDPFEYNKGQ--DFHIAGES	146	
QY	230	YGCHYCPAFNHYPYONERIANGSVNGVLNFSLGII--NGIIDEAIQAPYYEFA--	284		
Db			: : :		:
147	YAGHYIPVFASEILSHKDR-----NFNLTSVLINGLTDPLTOYNYEPMACGE	195			
QY	285	----VNNTYGIKAVNETVVNMKFANQMPPNGCQDLISTCKQNRRTALADYALCAEATNM	339		
Db			: : :		:
196	GGEPSVLPBEECSAMEDSL-----ERCLGHIESCYDSQ-----SWMSCVPATIY	239			
QY	340	CRDNVEGPPIYAFAGRGVYDIRHPYDD-----PTPPSYNFKFLAKDSVMDAIGVINYTQS	394		
Db			: : :	: : :	: : :
240	CNNAQLAPYQR-TGRNVYDIKDCCEGNLCYPTIQD-IDDYLNQDVTVKGAAGVADHYES	297			
QY	395	-NDVYAFQQTGGDFVMFNPIEDLEILALPVRSLSIYGDADYICNWFGGQAASLAANTS	453		
Db			: : :	: : :	: : :
298	CNFDLINRNFLFAGDMWK-P-YHTAVTDLLNQDLPILVYAGDKPICNLWLNKAWDVLPWK	356			
QY	454	QAQAFQRS---AGVTPLKVNGVEYGETREYCNFSFTFRVYEAGHEVPYQYIASIQLFNRTI	510		
Db			: : :	:~ : :	:~ : :
357	YDEEFASQKVRNWTASITDEVA-GEVKSXYKHFTYLTVFNGGHMVPDPDENALSIMVNEWI	415			
QY	511	FG 512			
Db		416 HG 417			

RESULT 9
US-10-425-114-48698
; Sequence 48698, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E

```

: APPLICANT: Cao, Yongwei
:
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
:
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
:
: FILE REFERENCE: 38-21(53313)B
:
: CURRENT APPLICATION NUMBER: US/10/425,114
:
: CURRENT FILING DATE: 2003-04-28
:
: NUMBER OF SEQ ID NOS: 73128
:
: SEQ ID NO 48698
:
: LENGTH: 500
:
: TYPE: PRT
:
: ORGANISM: Glycine max
:
: FEATURE:
:
: OTHER INFORMATION: Clone ID: 700563631_FLI.pcp
US-10-425-114-48698

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[illegible]

RESULT 10

```

US-10-425-114-44602
; Sequence 44602, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecu
; TITLE OF INVENTION: Plants and Uses Th
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

```

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; SEQ ID NO 44602
; LENGTH: 525
; TYPE: PRI
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701038279_FLI.pep
US-10-425-114-44602

Query Match          15.9%; Score 473; DB 12; Length 525;
Best Local Similarity 28.5%; Pred.No. 2e+35;
Matches 133; Conservative 77; Mismatches 182; Indels 74; Gaps 17;

Qy      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db      :|:|:~DSESVEDLGHAGYYPLOHSHAMRMFFFFESRNKED-PVVIWLTGGPGCSSELALFY 161
        :|:~ELGCHVNSTPDDYNPHSNWEVSNLLFLSQPLGVGFYSYSDTVDCGSINPVTCVVENSSPA 176
Qy      :|:~ENGPFKIADNLSLVMEYGDWKAASLLYVDQPTGTGFSYSSDLRDIRHNBEVG----- 214
        :|:~GVQGRYPIDATLDITTNLAEEAAEWIIQLGLSGLPSLDSRVOSKDFSLWTESYGHYGP 236
Db      :|:~-----SNDLYDTQAQFVEHP-----QYAKNDFFTGESYAGHYIP 250
        :|:~AFFNHFYQRNERIANGSYNGVLNFNSLGIIIDEAIQAPYYPEFAVNNTYGIKAVNE 296
        :|:~AFATRIHRGNK-----AKEGITHNLKGLAIGNLTNPALIQYKAYPDYALEMGI-IKKATR 304
Qy      :|:~TVNYMKFANMPNGCQDLISTCKQTNRTA-LADYALCAEATNCEDNVGEGYPAFAG-R 354
        :|:~LLNLIV-----LVPACEAISKLCTGNGKTSCMAAYVC---NVIFSDI---MLHAGDT 351
Qy      :|:~GVDIRHP-----YDDPTPPSYNNKFIAKDSVMDAIGV-NINYTOSNNDVVYAFQOTGD 407
        :|:~NYIDLRKCKEGLCYDF-----SNMOKFLNQQSVRSLSGVKHFVSCSTEVAAMLVD-- 405
Qy      :|:~FWPNFIE-DLREILALPVRSLLTYGDADIICNWFGQAVSLAANYSOAAQFRSAGYTPL 466
        :|:~WENLEVGIFDLEDGINLLVYAGEYDLICNWLNSRWVHAMWSGQKEFATSLEVVF 463
Qy      :|:~KVGVEYGETRYGNPSTRVTEAGHEVPYQPIASLQLFNRTIFG 512
        :|:~VVDGSEAGLLKSGYPLSFUKVHNAGHMVPMQDKAALEMCLKKWING 509

RESULT 11
US-10-437-963-155055
Sequence 155055, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 155055
LENGTH: 525
TYPE: PR
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(525)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Db 54 HAGYRLPRSKAARMFYFFFSR--SKNDPVVWILTGGPGSCSELALFYENGPFQLTKNL 112
 QY 128 DDIYNPHSWNEVSNLLFLSQPLGVGFSYSDTVDGSDNPVTGVVNSPAGVQGRYPTIDA 187
 Db 113 SLVWMDYGDWKAIIIFVDQPTGTGFSYSDSDIRHDEGV----- 154
 QY 188 TLIDITNLAAEAWEILQFLSGLSLDSRVOSKDFSLWTESYGGHYGPAFFNHFYEQNE 247
 Db 155 -----SNDLYDFLOAFFKEHP-----QFTKNDFYITGESYAGHYIPALASRVHOGNK 201
 QY 248 RIANGSVNGVQVNFNSLGIINGIIDEALQAPYYPFAVNTVGIKAVNETVYNYMKFANQ 307
 Db 202 -----AKGHIHNLKFGALNGLTNPEIQYQAYTDYALDR--GL--IKKAENSTI--NK 249
 QY 308 MPNGQDLSTC-KQTNRTALADYALCAEATNMCRDNVEGPPYAFAGRGVYDIRHP----- 362
 Db 250 LIPPCQAIEACGTEGGETCVSSLVVCKNIFNRIINTIADDVY-----YDIRKKCVGV 302
 QY 363 --YDDPTPPSYNKLAKDSVMDALGV--NINYTQSNNDVYAFQOTGDFVMPNFIE-DLE 418
 Db 303 LCYDF----SYMEDFLNEKTVRDALGVGLDFVSCSTVYSAMQD-----WNRNLEVGIP 354
 QY 419 EILALPVRVSLIYGADYVICKWFGQAVSLAANYSOAARFSAQYTPLVKNGVEYGETRE 478
 Db 355 TLLEGKVLVYAGEEDLICNWLGNRVRWQAMWESGQKQFASGTVPFLVDGAEAGTLKS 414
 QY 479 YGNFSTRVVBAGHEVPYQPIASLQLFNRITFG 512
 Db 415 HGPLAFLKVYEGAGHVMQDQPKAALMLRSMWQG 448

RESULT 13

US-10-382-239A-2
 ; Sequence 2, Application US/10382239A
 ; Publication No. US20030219511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Societe des Produits Nestle
 ; TITLE OF INVENTION: No. US20030219511A1el Carboxypeptidase of Cocoa
 ; FILE REFERENCE: 88265-7006
 ; CURRENT APPLICATION NUMBER: US/10/382,239A
 ; PRIOR FILING DATE: 2003-03-05
 ; PRIOR FILING DATE: EP 01116407.6
 ; PRIOR APPLICATION NUMBER: PCT/EP02/07162
 ; PRIOR FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 2
 ; LENGTH: 508
 ; TYPE: PRT
 ; ORGANISM: Theobroma cacao
 US-10-382-239A-2

Query Match 15.5%; Score 462.5; DB 15; Length 508;
 Best Local Similarity 27.5%; Pred. No. 1.9e-34;
 Matches 150; Conservative 88; Mismatches 203; Indels 105; Gaps 22;
 QY 4 YEF-LSVLPLVAASWA-----LPGSTPASVGRROL-----PKNPTGVKLTITA 45
 Db 8 YPFSVSLFLSISSAASFLDERLGGSSPFIHAKKLIRELNLPKKEENVV-----VDG 64
 QY 46 NNVTI-----RYKEPGAEGVCTTTPGVKS-----YSGY--VDTSPGSHTFPWFPE 88
 Db 65 GQVSLPEDSRVLEKREKFNEL-----AVPGSVSVELGHAGYKLANSHDARMFVFPE 119
 QY 89 ARHNPTAPITTLWANGPGSDSLIGLFBELGCHVNSTDDYINPHSWNEVSNLLFLSQP 148
 Db 120 SR-NSKQDPVWILTGGPGSCSELALFYENGPFPTIAENMSLIWNGQWMAASNLVVDQ 178
 QY 149 LGVGSYSYDVTGSDNPVTGVVNSPAGVQGRYPTIDATLDTTNLAAEAWEILQGL 208
 Db 179 IGTGFSYS-----SDRRDIRNEDEVSNLDYD-----FLOAFF 211

QY 209 SGLPSLDSRVOSKDFSLWTESYGGHYGPAFFNHFYEQNERIANGSVNGVQVNFNSLGIIN 268
 Db 212 AEHPFF-----EKNDFYITGESYAGHYIPAFARVHQGNK-----AKDGIHNLKGFAGN 262
 QY 269 GIIDEALQAPYYPFAVNTVGIKAVNETVYNYMKFANOMPNGCODLISTCKQTNR-TAL 327
 Db 263 GLTDPAIQYKAYTDYALD---MGVIKSDDNRI---NKLVPVCEMAIKLCTGDTGTISCM 315
 QY 328 ADYALCAEATNMCRDNVEGPPYAFAG-RGVYDIRHPYDDPTPPSYN--KFLAKDSVMDA 384
 Db 316 ASYFVC-----NAIFTGIMALAGDNYVDIRTKCGSSLCYDPSNMETFLNQSVRDA 367
 QY 385 IGV-NINYTQSNNDVYAFQOTGDFVMPNFIE-DLEEILALPVRVSLIYGADYICNWF 442
 Db 368 LGVGSIDFVSCSTVYQAMLYD---WNRNLEVGIPALLEDGVKLLVYAGEYDLICNWL 423
 QY 443 QCAVSLAANYSOAARFSAQYTPLVKNGVEYGETREYGNFSTRVYVEAGHVPYQPIAS 502
 Db 424 NSRWVHAMWESGQKEFVASPEVPFVVDGSEAGVLRTHGLGLFLKVDHAGHVMVMDQPKAA 483
 QY 503 LQLFNR 508
 Db 484 LEMLEK 489

RESULT 14

US-10-424-599-214407
 ; Sequence 214407, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 214407
 ; LENGTH: 484
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(484)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_35637C.1.pap
 US-10-424-599-214407

Query Match 15.4%; Score 458.5; DB 12; Length 484;
 Best Local Similarity 27.5%; Pred. No. 4.2e-34;
 Matches 150; Conservative 76; Mismatches 211; Indels 109; Gaps 22;
 QY 7 LSVLPLVAASW-----ALPGSTPASVGRROL-----PKNPTGV-----KTLTANN 47
 Db 5 VSLLLVLSLSFSYATSGFNHEHAYPPQSOAEMLTNLTNLPKDPVNIKIGDFDSDVFGKI 64
 QY 48 VTRVKEPGAEGVCTTTPGVKSYSYVDTSPGSHT-----FFWPFARHNPTAPITLWL 102
 Db 65 VEKFSLLGHSG-----PSIQHLGHAGQYSLPHSKAGSRFFVFESRNNKDD-PWVWL 118
 QY 103 NGCPGSDSLIGLFBELGCHVNSTDDYINPHSWNEVSNLLFLSQPLGVGSYSYDVTG 162
 Db 119 TGSPCGSELALFYENGPFPTIANNLSLTWYDYGWQASNLILFVDQPTGTGFSYSSD 177
 QY 163 INPVTGVVNSPAGVQGRYPTIDATLDTTNLAAEAWEILQGLSLGLPSLDSRVQSKD 222
 Db 178 IRRDEASISND-----LYDFLOEFFKAHP-----KRVKND 207
 QY 223 FSLWTESYGGHYGPAFFNHFYEQNERIANGSVNGVQVNFNSLGIINGIIDEALQAPYYPE 282

Db 208 FYITGESYAGHYTPAHASRIIQGNK-----ENOGIYINLKLGAIGNGATPAIQYQYPD 262
QY 283 FA-VNNTYGGIKAVNETVYNYMKFANOMPNGCODLISTCKQTNRTALADYALCAEATNMCR 341
Db 263 FAXLDNKKIITYA-----NDEINKLIPD-CEQAANTCETQGGOS-----CAIAFNTCQ 309
QY 342 -----DNVEGPPYAFAGRVYDIRHP-----YDDPTPSPSYNNKFLAKDSVMDAIGV- 387
Db 310 KIFVHILDFAFGINY-----YDIRKKCKGDMWCYDFRNVETLLN--LPK--VKSVIGVS 358
QY 388 -NINTQSNNDVYAFQGTGFVWPNFTIEDLEEILALPVRVSLYGDADYICNWFQGOAV 446
Db 359 NDLOVSVCSKRVHEAMQ--DYM-RNMEVEIPSLLEDGIKLVYVGBEDLICNWLGNRW 415
QY 447 SLAANYSQAAQFRSAGYTPLVKVGVEYGETREYGNFSTRVYEAGHEVPYYPQIASLQLF 506
Db 416 VHMKWSGKKAFGKSPTKVFVVDGSKAGSLNSYGLSPLKLVHEAGHLVPMQPKAALQML 475
QY 507 NRTIFG 512
Db 476 QSMWAG 481

Search completed: July 22, 2004, 21:29:56
Job time : 51 secs

345 LEKYLQKSVRDALGVGDIDFVSCSSTVYQA-----MLVDWMRNLE--VGIPALLEDG 395
QY 429 ---LIY-GDADYICNWFQGOAVSLAANYSQAAQFRSAGYTPLVKVGVEYGETREYGNFSF 484
Db 396 INMLVYAGEFDLICNWLGNKSWHAMEWSGQEFVVSSEVPFTVDDSEAGLLKKYGPISF 455
QY 485 TRVVEAGHEVPYYPQIASLQLFNR 508
Db 456 LKVDHAGHMVPMQPKASLEMLXR 479

RESULT 15
US-10-424-599-172991
; Sequence 172991, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 172991
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127226C.1.1.pep
US-10-424-599-172991

Query Match 15.3%; Score 455; DB 12; Length 499;
Best Local Similarity 29.1%; Pred.No.9.4e-34;
Matches 129; Conservative 68; Mismatches 175; Indels 72; Gaps 14;
QY 78 PESHT---PFWPFARHNPETAPITLWLNKGFGSDSLIGLFEELGCPCHVNSTFDDYINPH 134
Db 95 PHSHAAKMYFFPESR-NSKOPVVIWLTGGPGCSSELAVFYENGPFKIANNMSLWNVEY 153
QY 135 SNNEVSNLLFLSOPLGVSYSSTVDGSIINPTGVVENSFAGVQGRYPTIDATLIDTIN 194
Db 154 GMDKVNLLYVDQPTGTGFSYSTDKRDIRHDEGV-----188
QY 195 LAEEAAWETLQGLSLGSLDRVQSKDSFSLWTSYGGHYGPAPFNNHFEQNERIANGSV 254
Db 189 --SNDLYDFLQAFFAHP-----EYVKNDFITGESYAGHYIPAFARVHGNK-----AK 237
QY 255 NGVQLNFSLGIINGHIDEAIOAPYPYEPFANNYTGKAVNETVYNYMKFANOMPNGCQD 314
Db 238 EGIHINLKGPAIGNGLTDPGQYKAYTDYALDMGIIQKA-----DYERINKVWVPACEM 291
QY 315 LISTCKQTNRTA-LADYALCAEATNMCRDNVEGPPYAFAGRVYDIRHPYDDPTPSPYNN 373
Db 292 AIKLCGTGDKGIACCTASYFVCNTIFNSIMSHAGINY-----YDIRKKCEGSLCYDFS 344
QY 374 --KFLAKDSVMDAIGV-NINTQSNNDVYAFQGTGFVWPNFTIEDLEEILALPVRVS-- 428

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 29, 2004, 11:29:19 ; Search time 112 Seconds
(without alignments)
2749.980 Million cell updates/sec

Title: US-09-712-338-2
Perfect score: 2979
Sequence: 1 MRGVEFLSVLPVAAWALP.....HTQSSVPLPTATSMSSVGMA 555

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09712338/runat 22072004.170321.10374/app.query.fasta_1.711
-DB=Issued Patents NA -OPM=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09712338 @CGN 1 1 56 @runat 22072004.170321.10374 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2975	99.9	1662	3	US-08-943-714-1
2	623	20.9	2002	1	US-08-309-341-3
3	623	20.9	2002	1	US-08-608-267-3
4	623	20.9	2002	1	US-08-608-452-3
5	623	20.9	2002	1	US-08-608-224-3
6	623	20.9	2002	2	US-08-967-149-3
7	594	19.9	2068	1	US-08-309-341-1
8	594	19.9	2068	1	US-08-608-267-1
9	594	19.9	2068	1	US-08-608-452-1
10	594	19.9	2068	1	US-08-608-224-1
11	594	19.9	2068	2	US-08-967-149-1
12	568.5	19.1	2503	1	US-09-640-305-3

13	568.5	19.1	2503	1	US-08-360-673-3	Sequence 3, Appli
14	523.5	17.6	2632	2	US-08-899-324-32	Sequence 32, Appli
15	523.5	17.6	2632	3	US-08-329-892B-32	Sequence 32, Appli
16	361	12.1	1551	2	US-08-828-488-4	Sequence 4, Appli
17	361	12.1	1551	4	US-09-299-689A-4	Sequence 4, Appli
18	359	12.1	2076	4	US-09-907-794A-163	Sequence 163, App
19	359	12.1	2076	4	US-09-905-125A-163	Sequence 163, App
20	359	12.1	2076	4	US-09-902-775A-163	Sequence 2, Appli
21	348.5	11.7	1670	2	US-08-828-488-2	Sequence 319, App
22	348.5	11.7	1670	4	US-09-299-689A-2	Sequence 319, App
23	339.5	11.4	1814	4	US-09-702-705-319	Sequence 319, App
24	339.5	11.4	1814	4	US-09-736-457-319	Sequence 319, App
25	339.5	11.4	1814	4	US-09-614-124B-319	Sequence 319, App
26	339.5	11.4	1814	4	US-09-671-325-319	Sequence 319, App
27	339.5	11.4	1814	4	US-09-589-184-319	Sequence 6, Appli
28	275	9.2	1256	4	US-09-896-866B-6	Sequence 5, Appli
29	275	9.2	1302	4	US-09-896-866B-9	Sequence 9, Appli
30	275	9.2	1317	4	US-09-896-866B-9	Sequence 674, App
31	266.5	8.9	1071	4	US-09-023-655-674	Sequence 9, Appli
32	246.5	8.3	1604	1	US-08-665-966-9	Sequence 254, App
33	246.5	8.3	1604	3	US-09-041-780-9	Sequence 9, Appli
34	239.5	8.0	1650	4	US-09-907-794A-254	Sequence 254, App
35	239.5	8.0	1650	4	US-09-905-125A-254	Sequence 254, App
36	239.5	8.0	1650	4	US-09-902-775A-254	Sequence 6, Appli
37	169.5	5.7	1263	2	US-08-828-488-6	Sequence 133, App
38	169.5	5.7	1263	4	US-09-299-689A-6	Sequence 190, App
39	163	5.5	1960	4	US-09-280-116-133	Sequence 190, App
40	161.5	5.4	497	4	US-09-643-597-190	Sequence 190, App
41	161.5	5.4	497	4	US-09-480-884A-190	Sequence 190, App
42	161.5	5.4	497	4	US-09-542-615A-190	Sequence 190, App
43	161.5	5.4	497	4	US-09-606-421B-190	Sequence 131, App
44	154	5.2	357	4	US-09-280-116-131	Sequence 130, App
45	154	5.2	607	4	US-09-280-116-130	

ALIGNMENTS

RESULT 1
US-08-943-714-1
; Sequence 1, Application US/08943714
; Patent No. 6187578
; GENERAL INFORMATION:
; APPLICANT: Blinkovsky, Alexander
; APPLICANT: Berk, Randy
; APPLICANT: Rey, Michael
; APPLICANT: Golightly, Elizabeth
; APPLICANT: Klotz, Alan
; APPLICANT: Mathisen, Thomas Erik
; APPLICANT: Dammann, Claus
; TITLE OF INVENTION: Carboxypeptidases And Nucleic Acids
; TITLE OF INVENTION: Encoding Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 61875780 No. 6187578disk of No. 6187578th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,714
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4990.200-US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1662
OTHER INFORMATION:
US-08-943-714-1

Alignment Scores:
Pred. No.: 1, 21e-312 Length: 1662
Score: 2975.00 Matches: 554
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 3 Gaps: 0

US-09-712-338-2 (1-555) x US-08-943-714-1 (1-1662)

QY 1 MetArgGlyTyrGluPheLeuSerValLeuProLeuValAlaAlaSerTrpAlaLeuPro 20
Db 1 ATGGTGGCTACGAAATTTCTCAGTGTACCTTTGGTGGAGCCAGTTGGGCCCTTCCA 60
QY 21 GlySerThrProAlaSerValGlyArgGlnLeuProLysAsnProThrGlyVallys 40
Db 61 GGAAGTACACCGGCTCGGTAGAACAGACAGCTACCCAGAACCCACCGGGGTCAAG 120
QY 41 ThrLeuThrAlaAsnValThrIleArgTyrLysGluProGlyValadGlyVal 60
Db 121 ACTCTTACAAACCGCAACAAATGTCACCTCCGTTACAGAAACCCGGGGCAGAGGGCTC 180
QY 61 CysGluThrThrProGlyValLysSerTyrSerGlyTyrValAspThrSerProGluSer 80
Db 181 TCGAGACTACCCGGGTCTCAATCTACTCTGGATATGTGCACACCTCTCCCGAGTCC 240
QY 81 HisThrPheThrPheGluAlaArgHisAsnProGluThrAlaProIleThrLeu 100
Db 241 CATACCTTCTCTGGTCTTCCGAAGCAGACATAACCCAGAACTGCACCTATACATGG 300
QY 101 TrpLeuAsnGlyGlyProGlySerAspSerLeuLeGlyLeuPheGluLeuGlyPro 120
Db 301 TGGTTGAATGGTGGCCCTGGAACCGATTCTTTGATCGGTCTCTTGAAGAGTTGGCCCT 360
QY 121 CysHisValAsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSer 140
Db 361 TGCATGTCAATTTCGACTTTTGATGACTATACCAACCTCACTCTGCGGAACAGAGTCTCC 420
QY 141 AsnLeuPheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAsp 160
Db 421 AATTTACTATTCCTGCTCCAGCCATTGGGAGTCGGCTTTTCATATAGTAGACGGTIGAT 480
QY 161 GlySerIleAsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGly 180
Db 481 GGGTCCATTAAACCTGTAACTGGGGTCTGCGAAATTCGAGCTTTTCAGGAGTTTCAGGC 540
QY 181 ArgTyrProThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaGluAlaAla 200
Db 541 CGGTACCAACCACTTATGCACTCTGATCGATACCTACCAATCTTCCCGCAGAGCGCGCT 600
QY 201 TrpIleLeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSer 220
Db 601 TGGGAGATCTCTGAAGATTTCCTTAGTGAGTACCTAGCTTGGACTCTAGGGTGCAGTCT 660
QY 221 LysAspPheSerLeuTrpThrGluSerTyrGlyHisTyrGlyProAlaPheAsn 240
Db 661 AAGCACTTCAGTCTATGACGAGAGAGCTATGGAGGGCACTATGGTCTCTGATCTTCAAT 720

241 HisPheTyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsn 260
721 CATTTTACGAGCGAATGAGAAATGCCAACGGTAGTGTATTAATGCTGTACGCTTAAT 780
261 PheAsnSerLeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyr 280
781 TTCAACTCTCTGGGAATTAATAACGGCATCATCGACGAGCGATCCAGGCCCTTACTAC 840
281 ProGluPheAlaValAsnAsnThrTyrGlyIleIleAlaValAsnGluThrValTyrAsn 300
841 CCTGAATTCGCTGTGACAAATACCTACGGTATCAAGGCTGTCAAGGAGACCGTCTACAC 900
301 TyrMetLysPheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLys 320
901 TACATGAAGTTTGCACCAACCAATGCTGATGGTTCAGGATTTGATTTCCACCTGCAAA 960
321 GlnThrAsnArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCys 340
961 CAGACAAACCGCACCGCATTAGCTGACTAGCCCTCTGCGCCGAGCCACCAACATGTGC 1020
341 ArgAspAsnValGluGlyProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArg 360
1021 AGGACCAATGTTGAGGGGCCATACCTACGCTTTGCTGGTGTGTGTGTATGATATTCGG 1080
361 HisProTyrAspAspProThrProProSerTyrTyrAsnLysPheLeuAlaLysAspSer 380
1081 CATCATATGATGACCCGACTCCGCCAAGTTATTACAACAATTTCTGGCAAGACACTCT 1140
381 ValMetAspAlaIleGlyValAsnIleAsnTyrThrGlnSerAsnAspValTyrTyr 400
1141 GTCATGAGCGCTATCGGCTCAACATCAACTACACCCAGTCCCAATAATGACGCTCTAC 1200
401 AlaPheGlnGlnThrGlyAspPheValTrpProAsnPheIleGluAspLeuGluIle 420
1201 GCTTTCCAGCAACAGGCGACTTTGTCGGCCCACTTCATCGAAGACCTCGAGAGATC 1260
421 LeuAlaLeuProValArgValSerLeuIleTyrGlyAspAlaAspTyrIleCysAsnTrp 440
1261 CTGTGCTCTCCCGTGGCTCTCCCTCATCTATGCGCAGCGCGATTACATCTGCAACTGG 1320
441 PheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSerGlnAlaAlaGlnPheArgSer 460
1321 TTCGCGGTTCAGGCGGTTTCCCTCGCTCGCACTACTCCCAAGCCGCCAGTTCGGAAGC 1380
461 AlaGlyTyrThrProLeuLysValAsnGlyValGluTyrGlyGluThrArgGluTyrGly 480
1381 GCAGGTTACACCCCTGAAAGTCAACGCGCTCGAGTATGGGCAAACTCGCAGTATGCT 1440
481 AsnPheSerPheThrArgValTyrGluAlaGlyHisGluValProTyrTyrGlnProIle 500
1441 AATTTCTCTTCTCCTCGCTCTATGAGCAGCCCATGAAGTCCCATCTACAGGCCATC 1500
501 AlaSerLeuGlnLeuPheAsnArgThrIlePheGlyTrpAspIleAlaGlnGlyGlnLys 520
1501 GCCTCCCTGCAATTTGTTAACCGGACTATCTTCGTTGGGATATCGAGGGCCAGAG 1560
521 LysIleTrpProSerTyrLysThrAsnGlyThrAlaThrAlaThrHisThrGlnSerSer 540
1561 AAGATCTGCCCCAGCTTACAGAGCATGGAAACGGCTACAGCTACGATACAGATACAGTCT 1620
541 ValProLeuProThrAlaThrSerMetSerSerValGlyMet 554
1621 GTGCCGCTGCTACGCTACCGCTACCGCATGTCCAGTGTGGTATG 1662

RESULT 2
US-08-309-341-3
; Sequence 3, Application US/08309341
; Patent No. 5594119
; GENERAL INFORMATION:
; APPLICANT: Xaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER

; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NO. 55941190 No. 5594119disk of No. 5594119th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/309,341
 ; FILING DATE: 16-SEP-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney, Karen A.
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 4247.000-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2002 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: intron
 ; LOCATION: 349..411
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join (348..412)
 ; US-08-309-341-3

Alignment Scores:
 Pred. No.: 1,9e-57 Length: 2002
 Score: 623.00 Matches: 155
 Percent Similarity: 48.25% Conservative: 79
 Best Local Similarity: 31.96% Mismatches: 175
 Query Match: 20.91% Indels: 76
 DB: 1 Gaps: 18

US-09-712-338-2 (1-555) x US-08-309-341-3 (1-2002)

QY 45 AlaAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr 64
 DB 533 GCCTAGTACTAGGCTCAAGACCGGATCTCTCTGTCATC-----GAC 583
 QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerPro---GluSerHisThrPhe 83
 DB 584 CTGGCGTAAAGCAGTACACCGGTTATCTCGATGACACGAGAACGACGATCTGTTTC 643
 QY 84 PheTrpPheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsn 103
 DB 644 TACTGTTCTTCGAGTCTCGCAATACCGCGAGATGACCTGTTCTCTGTCGCTGAC 703
 QY 104 GlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluGlyProCysHisVal 123
 DB 704 GGTGGCCCTGGATGCTCTCCCTACCGGCTCTTTTCATGAGCTCGGCCCTAGCAGCATC 763
 QY 124 AsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuLeu 143
 DB 764 AACAAAGATCCAGCGGCTCTACACGACTAGCTTGAATCCMACCGCTCCGATGATC 823
 QY 144 PheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIle 163

DB 824 TTCCTTGACAGCCCTGTCAACGTCGGTTACTCTCTTACAGCAACTCTGCT----- 871
 QY 164 AsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrPro 183
 DB 871 ----- 871
 QY 184 ThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaGluAlaAlaTrpGluIle 203
 DB 872 -----GTACGCGACACCGTTGCTGTGCAAGGACGTCTATGCCCTTG 913
 QY 204 LeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPhe 223
 DB 914 CTTACCCCTCTTCTTCAACAACATTCCCC-----GAGTATGCCAAGCAGGACTTC 961
 QY 224 SerLeuTrpThrGluSerTyrGlyHisTyrGlyProAlaPhePheAsnHisPheTyr 243
 DB 962 CACATTGCGGTGAATCTCTATGCTGTGTCATATATCCCCGCTTTGCTCGGAGATTTTG 1021
 QY 244 GluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSer 263
 DB 1022 TCTCACAAGAGCGC-----AACATCAACCTCGAGTCC 1054
 QY 264 LeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPhe 283
 DB 1055 GTTCTTATGGCAACGGTCTCACCGACGGTCTCACTCAGTACGAGTACTACCGTCCCATG 1114
 QY 284 AlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLys 303
 DB 1115 GCCTGTGTGTCACGGT---GGTTACCCAGCTGCTTGACGAG---GGCTCTGCCAGGCC 1168
 QY 304 PheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsn 323
 DB 1169 ATGGACAACGCCCTTCTCTCGC---TGCCAGTCTATGATTGAGTCTTGTCTATAGTCCGAG 1225
 QY 324 ArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsn 343
 DB 1226 AGCGCT-----TGGGTTTGTCTCCCGCCTCCCATCTACTCTAACAACGCC 1270
 QY 344 ValGluGlyProTyrTyrAlaPheAlaGlyValTyrAspIleArgHisProTyr 363
 DB 1271 CTCCTTGGCCCTTACCAGCGC---ACCGGACAGAAAGTCTACGATGTTCTGGTAAAGTGC 1327
 QY 364 AspAspPro-----ThrProProSerTyrTyrAsnLysPheLeuAlaLys 378
 DB 1328 GAGGATAGCTCCAACCTCTGCTACTCGGCCATGGGTACGTACGAGTACCTCTGAACAAG 1387
 QY 379 AspSerValMetAspAlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsnAsp 397
 DB 1388 ACGAGTCTATTGAGGCTGTGTGGCGTGAAGTCAACGGCTACGACTCGTGCAACTTTGAC 1447
 QY 398 ValTyrTyrAlaPheGlnGlnThrGlyAspPheValTyrPro-----AsnPheIleGlu 415
 DB 1448 ATCAACCGCAACTCTCTCTCCACGGTGAAGTGAAGCCCTACACCGTCTCGTTCGG 1507
 QY 416 AspLeuGluGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAspAla 434
 DB 1508 GGACTCCTGGAG-----CAGATCCCTGTC-----CTGATCTACGCTGGTGAAGCC 1552
 QY 435 AspTyrIleCysAsnTrpPheGlyGlnAlaValSerLeuAlaAlaAsnTyrSerGln 454
 DB 1553 GATTTCATCTGCACTGGCTGGGCAACAGGCTCGACTGAAGCCCTTGAGTGGCCCGGA 1612
 QY 455 AlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal-----Asn 469
 DB 1613 CAGGCTGAATAGCTCCGCTAAGCTGGAGGACCTGGTGGTGGTGAAGTGAAGCAGCAG 1672
 QY 470 GlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGlu 489
 DB 1673 GCAAGAAAGATCGGCGCAGGTCAAGTCCCACTTCACTTCCATGCTCTCTATGCG 1732
 QY 490 AlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArgThr 509
 DB 1733 GGTGGCCACATGGTCCCGATGGACCAACCCGAGTCTTGAATTTCTTCAACCGCTGG 1792

QY	510	IlePheGly---Tyr	513	
Db	1793	TTGGGAGGTGAATGG	1807	
RESULT 3				
US-08-608-267-3				
Sequence 3, Application US/08608267				
Patent No. 5688663				
GENERAL INFORMATION:				
APPLICANT: Yaver, Debbie Sue				
APPLICANT: Thompson, Sheryl Ann				
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER				
NUMBER OF SEQUENCES: 4				
CORRESPONDENCE ADDRESS:				
ADDRESS: NO. 56886630 No. 5688663disk of No. 5688663th America, Inc.				
STREET: 405 Lexington Avenue, Suite 6400				
CITY: New York				
STATE: New York				
COUNTRY: U.S.A.				
ZIP: 10174-6401				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/608,267				
FILING DATE: 28-FEB-1996				
CLASSIFICATION: 435				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 08/309,341				
FILING DATE: 20-SEP-1994				
ATTORNEY/AGENT INFORMATION:				
NAME: Lowney, Karen A.				
REGISTRATION NUMBER: 31,274				
REFERENCE/DOCKET NUMBER: 4247,000-US				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: 212 867 0123				
TELEFAX: 212 867 0298				
INFORMATION FOR SEQ ID NO: 3:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 2002 base pairs				
TYPE: nucleic acid				
STRANDEDNESS: double				
TOPOLOGY: linear				
MOLECULE TYPE: cDNA				
ORIGINAL SOURCE:				
ORGANISM: Aspergillus niger				
FEATURE:				
NAME/KEY: intron				
LOCATION: 349..411				
FEATURE:				
NAME/KEY: CDS				
LOCATION: join (348..412)				
US-08-608-267-3				
Alignment Scores:				
Pred. No.:	1-9e-57	Length:	2002	
Score:	623.00	Matches:	155	
Percent Similarity:	48.25%	Conservative:	79	
Best Local Similarity:	31.96%	Mismatches:	175	
Query Match:	20.91%	Indels:	76	
DB:	1	Gaps:	18	
US-09-712-338-2 (1-555) x US-08-608-267-3 (1-2002).				
QY	45	AlaAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr	64	
Db	533	GCCTATGATCTCAGGGTCAAGAGACCGATCTAGTCTCTTGGCATC-----GAC	583	
QY	65	ProGlyValLysSerTyrSerGlyTyrValAspThrSerPro---GluSerHisThrPhe	83	

QY 435 AspyrilleCysAsnTrpPheGlyGlnAlaValSerLeuAlaAAsnTyrSerGln 454
 Db 1553 GATTTCATCTGCACTGGCTGGCAACAGGCTGAGTGAAGCTTCTGAGTGGCCCGGA 1612
 QY 455 AlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal-----Asn 469
 Db 1613 CAGGCTGAATATGCTCCGCTAAGCTGAGGAGCTGGTGGTGGAGATGAGCACAAG 1672
 QY 470 GlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGlu 489
 Db 1673 GGCAAGAGATCGCCAGCTCAAGTCCATGGCACTTCACTTCATCGCTCTATGGC 1732
 QY 490 AlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArgThr 509
 Db 1733 GGTGGCCACATGCTCCGATGAGCAACCCGAGTGGTCTTGATTTCTTCAACCGCTGG 1792
 QY 510 IlePheGly---Trp 513
 Db 1793 TTGGGAGGTGAATGG 1807
 RESULT 4
 US-08-608-452-3
 : Sequence 3, Application US/08608452
 : Patent No. 5693510
 : GENERAL INFORMATION:
 : APPLICANT: Yaver, Debbie Sue
 : APPLICANT: Thompson, Sheryl Ann
 : TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: No. 56935100 No. 5693510disk of No. 5693510th America, Inc.
 : STREET: 405 Lexington Avenue, Suite 6400
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10174-6401
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/608,452
 : FILING DATE: 28-FEB-1996
 : CLASSIFICATION: 536
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: US 08/309,341
 : FILING DATE: 20-SEP-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lowney, Karen A.
 : REGISTRATION NUMBER: 31,274
 : REFERENCE/DOCKET NUMBER: 4247,000-US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 212 867 0123
 : TELEFAX: 212 867 0298
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2002 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : ORIGINAL SOURCE:
 : ORGANISM: Aspergillus niger
 : FEATURE:
 : NAME/KEY: intron
 : LOCATION: 349..411
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: Join (348..412)
 : US-08-608-452-3

Alignment Scores:
 Pred. No.: 1.9e-57 Length: 2002
 Score: 623.00 Matches: 155
 Percent Similarity: 48.25% Conservative: 79
 Best Local Similarity: 31.96% Mismatches: 175
 Query Match: 20.91% Indels: 76
 DB: 1 Gaps: 18
 US-09-712-338-2 (1-555) x US-08-608-452-3 (1-2002)
 QY 45 AlaAsnAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr 64
 Db 533 GCCTATGATCTCAGGTCAGAGACCGCTCTAGCTCTCTTGGCATC-----GAC 583
 QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerPro---GluSerHisThrPhe 83
 Db 584 CCTGGCTAAAGCAGTACACCGGTTATCTCGATGACACGACGACGACGACATCTGTTTC 643
 QY 84 PheTrpPhePheGluAlaArgHisAsnProGluThrAlaProIleThrLeuThrLeuAsn 103
 Db 644 TACTGGTTCTTCGAGTCTCGCAATGACCCGAGAAATGACCTGTGTCTGTGCTGAAC 703
 QY 104 GlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluGlyProCysHisVal 123
 Db 704 GTGGCCCTGGATGCTCTTCCCTACCGGTTTTCATGAGCTCGGCCCTAGCAGATC 763
 QY 124 AsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuLeu 143
 Db 764 AACAAAGATCCACGCGGTCTACAAGCTACGCTGGAACTCCACGCGTCCGTCATC 823
 QY 144 PheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIle 163
 Db 824 TTCTTTGACCGCTGCTTCAACGTCGGTTACTCTTACAGCAACTCTGCT----- 871
 QY 164 AsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrPro 183
 Db 871 ----- 871
 QY 184 ThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaAlaGluAlaLalTrpGluIle 203
 Db 872 -----GTCAGCAGACCGTGTGCTGGCAGGAGCGTCTATGCTTG 913
 QY 204 LeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPhe 223
 Db 914 CTTACCTCTTCTTCAACAATTCCTCC-----GAGTATGCCAAGCAGGACTTC 961
 QY 224 SerLeuTrpThrGluSerTyrGlyGlyHisTyrGlyProAlaPhePheAsnHisPheTyr 243
 Db 962 CACATTCGCGGTGAATCTTATGCTGTCTATATCCCGCTCTTCTGCGGAGATTTTG 1021
 QY 244 GluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSer 263
 Db 1022 TCTCACAAGAAGCGC-----AACATCAACTGACGAGTCC 1054
 QY 264 LeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPhe 283
 Db 1055 GTCTTATTTGGCAACGGTCTCACCGCGTCTCTCACTCAGTACGAGTACTTACCGTCCCATG 1114
 QY 284 AlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLys 303
 Db 1115 GCCTGTGTGACGGT---GGTTACCCAGCTGCTTGGAGCAG---GGTCTCTCCGAGGCC 1168
 QY 304 PheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsn 323
 Db 1169 ATGGACAACGCCCTTCTCTCGC---TGCCAGCTATGATGAGTGTGCTGTATAGTTCGAG 1225
 QY 324 ArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsn 343
 Db 1226 AGCGCT-----TGGGTTTGTGTCCCGGCTCCATCTACTGTAAACAACGCC 1270
 QY 344 ValGluGlyProTyrThrAlaPheAlaGlyArgGlyValTyrAspIleArgHisProTyr 363
 Db 1271 CTCCTTGCCCTTACCGCGC---ACCGGACAGAAGCTCTACGATGTTCTGTTAAGTGC 1327


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QY 284 AlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLys 303
D 1115 GCCTGTGTGACGGT---GGTTACCCAGCTCTTGGACGAG---GGCTCTCCGACGCC 1168
QY 304 PheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsn 323
D 1169 ATGACAAACGCCCTTCCTCGC---TGCCAGTCTATGATTGAGTCTTGCTATAGTTCGAG 1225
QY 324 ArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsn 343
D 1226 AGCGCT-----TGGTTGTGTCCGCCCTCCATCTACTACTGTAAACAAGGCC 1270
QY 344 ValGluGlyProTyrTyrAlaPheAlaGlyValTyrAspIleArgHisProTyr 363
D 1271 CTCCTTCCCTTACCAGCGC---ACCGACAGACAGCTTACGATGTTCTGGTAAAGTC 1327
QY 364 AspAspPro-----ThrProSerTyrTyrAsnLysPheLeuAlaLys 378
D 1328 GAGGATAGCTCCACCTCTCTACTCGCCATGGCTACGTCAGCGACTACCTGAACAAG 1387
QY 379 AspSerValMetAspAlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsp 397
D 1388 ACCGAGTCAATTGAGGCTGTGGCTGAGTCAACGGCTACGACTCGTGCACCTTTGAC 1447
QY 398 ValTyrTyrAlaPheGlnGlnThrGlyAspPheValTyrPro-----AsnPheIleGlu 415
D 1448 ATCAACCGCAACTCTCTTCCACGGTGACTGGATGAAGCCCTACCAACCGCTCTGTTCCG 1507
QY 416 AspleuGluGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAspAla 434
D 1508 GGACTCTCTGGAG-----CAGATCCCTGTC-----CTGATCTACGCTGTGACGCC 1552
QY 435 AspTyrIleCysAsnTyrPheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSerGln 454
D 1553 GATTCATCTGCACTGGCTGGGCAACAGCGCTGGACTGAAGCCCTTGAGTGCGCCGGA 1612
QY 455 AlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal-----Asn 469
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QY 470 GlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGlu 489
D 1673 GGCAAGAAGATCGCCAGGTCAAAGTCCCATGGCAACTTCACTTCATGCTCTCTATGGC 1732
QY 490 AlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArgThr 509
D 1733 GTGGCCACATGTTCCGATGGACCAACCCGAGTCGAGTCTTGAAATTTTCAACCGCTGG 1792
QY 510 IlePheGly---Trp 513
D 1793 TTGGGAGGTGAATGG 1807

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RESULT 6

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US-08-967-149-3
; Sequence 3, Application US/08967149
; Patent No. 5939305
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939305o No. 5939305disk of No. 5939305th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,149
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,452
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 349..411
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (348..412)
; US-08-967-149-3

Alignment Scores:
Pred. No.: 1-9e-57 Length: 2002
Score: 623.00 Matches: 155
Percent Similarity: 48.25% Conservative: 79
Best Local Similarity: 31.96% Mismatches: 175
Query Match: 20.91% Indels: 76
DB: 2 Gaps: 18

US-09-712-338-2 (1-555) x US-08-967-149-3 (1-2002)

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D 533 GCCTATGATCTCAGGGTCAAGAAGACCGATCCTAGCTCTTGGCATC-----GAC 583
QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerPro---GluSerHisThrPhe 83
D 584 CTGGCGTAAAGCAGTACACCGGTTATCTCGATGACACGAGAACCGAAGCATCTGTTTC 643
QY 84 PheTyrPhePheGluAlaArgHisAsnProGluThrAlaProIleThrLeuThrPheAsn 103
D 644 TACTGGTCTTCGAGTCTCGCATGACCCGAGAAATGACCCCTGTTCTTGGCTGAAC 703
QY 104 GlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHisVal 123
D 704 GGTGGCCCTGGATGCTTCTCCCTACCGGCTCTTTTCATGAGCTCGGCCCTAGCAGCATC 763
QY 124 AsnSerThrPheAspAspTyrIleAsnProHisSerTyrAsnGluValSerAsnLeuLeu 143
D 764 AACAAAGAAGATCCAGCCGGTCTTACACGACTACGCTTGGAACTCCAAACGCGCTCGTATC 823
QY 144 PheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIle 163
D 824 TTCCTTGACCGCTGTCAACGTCGTTACTCTTACAGCACTCTGCT-----871
QY 164 AsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrPro 183
D 871 -----871

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QY	184	ThrIleAspAlaThrLeuIleAspThrAsnLeuAlaAlaGluAlaAlaTrpGluIle	203
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QY	204	LeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPhe	223
Db	914	CTTACCTCTCTTCAACAATTCCTCC	961
QY	224	SerLeuTrpThrGluSerTyrGlyGlyHisTyrGlyProAlaPhePheAsnHisPheTyr	243
Db	962	CACATTGCGGTGAATCTATGCTGTGCTACTATATCCCGCTTTGCTGCGAGATTGTG	1021
QY	244	GluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSer	263
Db	1022	TCTCACAGAGAGCGC	1054
QY	264	LeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPhe	283
Db	1055	GTTCCTATTGGCAAGGCTCTACCGAGGTCTCACTCAGTACGAGTACTACCGTCCCATG	1114
QY	284	AlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLys	303
Db	1115	GCCTGTGTGACGGT--GGTTACCCAGCTGTCTGGACGAG--GGCTCTGCGCAGGCC	1168
QY	304	PheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsn	323
Db	1169	ATGGACACACGCCCTTCCTCGC--TGCCAGCTCTATGATGTAGTCTTGCTATAGTTCCGAG	1225
QY	324	ArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsn	343
Db	1226	AGCGCT--TGGTTGTGTCCCGGCTCCACTACTGTATAACACGCC	1270
QY	344	ValGluGlyProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisProTyr	363
Db	1271	CTCCTTGCCCTTACCAGCGC--ACCGACACACGCTACGATGTTCTGTGTAAGTGC	1327
QY	364	AspAspPro-----ThrProSerTyrTyrAsnLysPheLeuAlaLys	378
Db	1328	GAGGATAGCTCAACCTCTGCTACTCGGCCATGCGGCTACGTCAGCGACTACTGTACAAAG	1387
QY	379	AspSerValMetAspAlaIleGlyValAsnIleAsn--TyrThrGlnSerAsnAsnAsp	397
Db	1388	ACCGAGGTCATGAGGCTGTGGCGCTGAGGTCAACGGCTACGACTCGTGCACATTTGCAC	1447
QY	398	ValTyrTyrAlaPheGlnThrGlyAspPheValTrpPro-----AsnPheIleGlu	415
Db	1448	ATCAACCGCAACTTCTCTTCCACGGTGAATGATGAAGCCCTACACCGCTCTCGTTCGG	1507
QY	416	AspLeuGluGluIleLeuAlaLeuProValArgValSerLeuIleTyr--GlyAspAla	434
Db	1508	GGACTCTCTGGAG--CAGATCTCTCTGTC-----CTGATCTAGCTGTGTCAGCGCC	1552
QY	435	AspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAsnTyrSerGln	454
Db	1553	GATTTCACTGCAACTGGCTGGCAACAGCGCTGCACTGAAGCCCTTGAGTGGCGCGGA	1612
QY	455	AlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal-----Asn	469
Db	1613	CAGGCTGAATATGCTCCGCTAAGCTGGAGGACCTGGTGTGTCGAGAAATGAGCACAAAG	1672
QY	470	GlyValGluTyrGlyLeuThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGlu	489
Db	1673	GGCAAGAAATCGGCAGGTCAAGTCCCATGGCACTTCACTTATGCGTCTCTATGCG	1732
QY	490	AlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArgThr	509
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QY	510	IlePheGly---Trp	513
Db	1793	TTGGGAGGTGAATGG	1807
RESULT 7			

US-08-309-341-1

Sequence 1, Application US/08309341

Patent No. 5594119

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Thompson, Sheryl Ann

TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 55941190 No. 5594119disk of No. 5594119th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/08/309,341

APPLICATION NUMBER: US/08/309,341

FILING DATE: 16-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lowney, Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4247.000-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2068 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORGANISM SOURCE: Aspergillus niger

FEATURE:

NAME/KEY: intron

LOCATION: 572..632

FEATURE:

NAME/KEY: CDS

LOCATION: join (571..633)

US-08-309-341-1

Alignment Scores:

Pred. No.: 2,79e-54

Length: 2068

Score: 594.00

Matches: 155

Percent Similarity: 46.44%

Conservative: 80

Best local Similarity: 30.63%

Mismatches: 174

Query Match: 19.94%

Indels: 98

DB: 1

Gaps: 18

US-09-712-338-2 (1-555) x US-08-309-341-1 (1-2068)

QY 45 AlaAsnAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr 64 || Db | 457 GCCTATGATCTCAGGCTCAAGAAGCCGATCTGCTCTCTTGGCATC-----GAC | 507 |
QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerProGlu-----	79	
Db	508 CCCGCGGTGAACAGTACACCGTTATCTCGATGACACGA-GAATGATAGCATTTGTT	566
QY 80 -----SerHisThrPhePhe-----	84	
Db	567 CTACGTAAGCACACCTTGTTCAAGATCACGCTTTTATATCTCTGATATCTTAACGCA	626
QY 85 -----TrpPheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeu	102	
Db	627 ACTTAGTGGTTCTTCGAGTCTCGCAATGACCCCGAATGATGATCCCGCTGCTG	686

QY 103 AsnGlyGlyProGlySerAspSerLeuLeuLeuLeuLeuLeuGlyProCysHis 122
 DB 687 AACGGTGGCGTGGTGGTCTTCCTCCCTCACCAGTCTCTCATGGAGCTTGGCCCTAGCAGC 746
 QY 123 ValAsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeu 142
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 QY 243 TyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsn 262
 DB 1005 CTGTCTCACAGAAGCGC-----AACATCAACCTGCAG 1037
 QY 263 SerLeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGlu 282
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 DB 1158 GAC-----AACGCTCTTCTCCGCG-----TGCCAGTCTATGATGCTGCTACAGTCC 1208
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 DB 1254 GCCCTCTTGGCCCTTACCAGCGC---ACTGGGCGAGACGCTCTATGATGCTGCTGTAAG 1310
 QY 363 TyrAspAspPro-----ThrProProSerTyrTyrAsnLysPheLeuAla 377
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 QY 378 LysAspSerValMetAspAlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsn 396
 DB 1371 AAGCCGAGTATATCAGAGCTGTGGCGTGTAGGTCAACGGCTACGACTCGTGCACCTTT 1430
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 DB 1431 GACATCAACCGCAACTCTCTTCCAGGCTGTGGCTGAGTCAACGGCTACGACTCGTGCACCTTT 1490
 QY 415 GluAspLeuGluLeuLeuAlaLeuProValArgValSerLeuIleTyr---GlyAsp 433
 DB 1491 CCGGAGCTCTCGAG-----CAGATCCCTGTC-----TTGATCTATGCGGTGAT 1535
 QY 434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAsnTyrSer 453
 DB 1536 GCTGATTCTTTCGACTGGTGGGCAACAAGGCTGAGTGAAGCCCTGGAGTGGCCC 1595

QY 454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal----- 468
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 QY 489 GluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArg 508
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 RESULT 8
 US-08-608-267-1
 ; Sequence 1, Application US/08608267
 ; Patent No. 5688663
 ; GENERAL INFORMATION:
 ; APPLICANT: Yaver, Debbie Sue
 ; APPLICANT: Thompson, Sheryl Ann
 ; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5688663o No. 5688663disk of No. 5688663th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/608,267
 ; FILING DATE: 28-FEB-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA: US 08/309,341
 ; FILING DATE: 20-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney, Karen A.
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 4247.000-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2068 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: intron
 ; LOCATION: 572..632
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join (571..633)
 ; US-08-608-267-1
 Alignment Scores:
 Pred. No.: 2,79e-54 Length: 2068
 Score: 594.00 Matches: 155
 Percent Similarity: 46.44% Conservative: 80
 Best Local Similarity: 30.63% Mismatches: 174

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Query Match: 19.94% Indels: 98
DB: 1 Gaps: 18

US-09-712-338-2 (1-555) x US-08-608-267-1 (1-2068)

QY 45 AlaAsnValThrIleAspGlyValGluGlyValCysGluThrThr 64
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QY 65 ProGlyValLysSerThrSerGlyThrValAspThrSerProGlu-----79
DB 508 CCCGGCTGAAGCATACACCGGTTAICTCGATCACAACGA-GAATGATAAGCATTTGTT 566
QY 80 -----SerHisThrPhePhe-----84
DB 567 CTACGTAAACACACCTTGGTTCAAGATCACGCTTTTATATGCTCTGGATATCAACGCA 626
QY 85 -----TrpPheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTyrLeu 102
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DB 747 ATCAACAAGAGATCCAGCCGGTCTACAAATGACTACGCTTGGAACTCCACGCGTCCGTG 806
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DB 1038 TCGTCTCTATGGCAACGGTCTCACCGGAGGATACACCCAGTACGAGTACCTGCTGCC 1097
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DB 1098 ATGGCTCGGTGACGCGGCTTACCCAGCTGCTTGGAGGAGAGCTCTGCCACGCTCATG 1157
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DB 1209 GAGAGCGCT-----TGGGTTGTGTCGCGGCTCCATCTACTGTAACAAC 1253
QY 343 AsnValGluGlyProTyrTyrAlaPheAlaGlyValTyrAspIleArgHisPro 362
DB 1254 GCCTCTCTGCTTCCCGCTTACCGCGC-----ACTGGGCAAGACGCTATGATGTCGCTGTAAG 1310

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363 TyrAspAspPro-----ThrProProSerTyrTyrAsnLysPheLeuAla 377
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DB 1371 AAGCCCGAAGTATCATCAGAGCTGTGGCGCTGAGGTCACCGCTACGACTCGTGCACATTT 1430
QY 397 AspValTyrTyrAlaPheGlnThrGlyAspPheValTyrPro-----AsnPheIle 414
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QY 434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSer 453
DB 1536 GCTGATTTCTATTGCAACTGGTGGCAACAAGCGCTGGAGCTGAAGCCCTGGAGTGGCCC 1595
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QY 509 ThrIlePheGly---Trp 513
DB 1776 TGGTTGGAGGTGATGG 1793

RESULT 9
US-08-608-452-1
; Sequence 1, Application US/08608452
; Patent No. 5693510
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56935100 No. 5693510disk of No. 5693510th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
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; STATE: New York
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; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2068 base pairs
; TYPE: nucleic acid
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; TOPOLOGY: linear
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; ORGANISM: Aspergillus niger
; FEATURE:
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;   LOCATION: 572..632
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: join (571..633)
; US-08-608-452-1
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Pred. No.: 2,79e-54 Length: 2068
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Query Match: 19.94% Indels: 98
DB: 1 Gaps: 18

US-09-712-338-2 (1-555) x US-08-608-452-1 (1-2068)
QY 45 AlaAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr 64
DB 457 GCCTATGATCTCAGGTCACAGACCGATCCCTGGCTCTCTTGGCATC-----GAC 507
QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerProGlu-----79
DB 508 CCGGGCTGAAGCAGTACACCGGTATCTCGATGACAAAGA-GAATGATAAGCATTTGTT 566
QY 80 -----SerHisThrPhePhe-----84
DB 567 CTACGTAAGCACACCTTGGTTCAGATCACGCTTTTATATGCTCTGGATATCAACGCA 626
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QY 143 LeuPheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySer 162
DB 807 ATCTTCCTTGACGAGCTGCAATGTGGGTACTCTCTACGTAACCTCTGCT-----857
QY 163 IleAsnProValThrGlyValGluValGluAsnSerSerPheAlaGlyValGlnGlyArgTyr 182
DB 857 -----857
QY 183 ProThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaAlaGluAlaThrGlu 202
DB 858 -----GTCAGCGACACGGTCTGCTGGCAAGGACGCTCTATGTC 896
QY 203 IleLeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAsp 222
DB 897 TTGCTTACCTCTCTTCAACAATTCCTC-----GAGTATGCTAAGCAGGAC 944
QY 223 PheSerLeuThrThrGluSerTyrGlyHisTyrGlyProAlaPheAsnHisPhe 242
DB 945 TTCCACATTCGGGTGAATCTTATGTGTGCTACTATATCCCGTCTTCCTTCGGAGATC 1004
QY 243 TyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsn 262
DB 1005 CTGTCTCTCAAGAAGCGC-----AACATCAACCTGCAG 1037

263 SerLeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGlu 282
1038 TCGTTCTTCATTGGCAACGGTCTCACCGAGGATACACCCAGTAGTACTACCGTCCC 1097
283 PheAlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMet 302
1098 ATGCGCTGGCGTGACGGCGGTTACCCAGCTGTCTTGGCAGAGAGCTCCTCCGACATCCATG 1157
303 LysPheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThr 322
1158 GAC-----AACGCTCTTCTCTCGC---TGCCAGTCTATGATTGAGTCTTGTCTACAGTTC 1208
323 AsnArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAsp 342
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343 AsnValGluGlyProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisPro 362
1254 GCCTCTCTTCCCTTACAGCGC---ACTGGCGAGAACGCTCTATGATGTCCGTGGTAAG 1310
363 TyrAspAspPro-----ThrProSerTyrTyrAsnLysPheLeuAla 377
1311 TCGGAGGATAGCTCTAACCTTTGCTACTCGCTATGGCTACGTCAGGACTACCTGAAC 1370
378 LysAspSerValMetAspAlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsn 396
1371 AAGCCCGAAGTCTACGAGGCTGTGGCGTGTAGGTCAACGGCTACGACTCGTCAACTTT 1430
397 AspValTyrTyrAlaPheGlnGlnThrGlyAspPheValTrpPro-----AsnPheIle 414
1431 GACATCAACCGCAACTCTCTTCCAGGTGATGATGAAGCCCTACCAACCGCTCGTT 1490
415 GluAspLeuGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAsp 433
1491 CCGGAGCTCTCGAG-----CAGATCCCTGTC-----TTGATCTATGCGGTGAT 1535
434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAsnTyrSer 453
1536 GCTGATTTTCATTGCAACTGGCTGGGCAACAAGCGCTGGACTGAAGCCCTGGAGTGGCCC 1595
454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal-----468
1596 GGACAGCTGAAATATGCTCCGCTGAGCTGGAGGATCTGGTATCTTCGCAATGAGCAC 1655
469 AsnGlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyr 488
1656 ACGGGCAAGAAAGATTGGCCAGGTAAAGTCCCATGGCAACTTCACCTTCATGGTCTCTAT 1715
489 GluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArg 508
1716 GGTGGTGGCCACATGCTGCCGATGGACCGCGAGTCGAGTCTCGAGTCTTCGATTTCAACCGC 1775
509 ThrIlePheGly---Tyr 513
1776 TGGTTGGGAGGTGAATGG 1793

RESULT 10
US-08-608-224-1
; Sequence 1, Application US/08608224
; Patent No. 5705376
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57053760 No. 5705376disk of No. 5705376th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,224
FILING DATE: 28-FEB-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.

REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-608-224-1

Alignment Scores:
Pred. No.: 2,79e-54 Length: 2068
Score: 594.00 Matches: 155
Percent Similarity: 46.44% Conservatives: 80
Best local Similarity: 30.63% Mismatches: 174
Query Match: 19.94% Indels: 98
DB: 1 Gaps: 18

US-09-712-338-2 (1-555) x US-08-608-224-1 (1-2068)

QY 45 AlaAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr 64
Db 457 GCCTATGATCTCAGGGTCAAGAAGACCGATCGTGGCTCTCTTGGCATC-----GAC 507
QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerProGlu----- 79
Db 508 CCCGCGTGAAGCAGTACACCGGTTATCTCGATGACACGA-GAATGATAGCATTTGTT 566
QY 80 -----SerHisThrPhePhe----- 84
Db 567 CTACGTAGACACACCTTGGTTCAGATCAGCGTTTATATGCTCTGGATATCTAACGCA 626
QY 85 -----TrpPheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeu 102
Db 627 ACTTAGTGGTTCTCGAGTCTCGAATGACCCGAGATGATCCCGGTTGTTCTGTGGCTG 686
QY 103 AsnGlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHis 122
Db 687 AACGGTGGCCCTGGGTGCTCTCCCTACCGGTCTCTTCATGAGAGCTTGGCCCTAGCAGC 746
QY 123 ValAsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeu 142
Db 747 ATCAACAGAGAGATCCAGCGGTCTACATGATGATGAGCTTGGAACTCCAAACCGTCCGCTG 806
QY 143 LeuPheLeuSerGluProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySer 162
Db 807 ATCTTCTTGACGAGCCCTGCAATGCTGGTTACTCTACAGTAATCTGCT----- 857

QY 163 IleAsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyr 182
Db 857 ----- 857
QY 183 ProThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaGluAlaAlaTrpGlu 202
Db 858 -----GTACGCGACACGCGTCTGCTGGCAAGGAGGAGCTGTATGCC 896
QY 203 IleLeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAsp 222
Db 897 TTGCTTACCCTCTCTTCAACAATTCCTCC-----GAGTATGTAAGCAGACGAC 944
QY 223 PheSerLeuTrpThrGluSerTyrGlyGlyHisTyrGlyProAlaPheAsnHisPhe 242
Db 945 TTCACATTCGCGGTGAATCTTATGCTGTCACCTATATCCCGCTTCGCTTCGAGATC 1004
QY 243 TyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsn 262
Db 1005 CTGTCTCACAGAAGAGCG-----AACATCAACCTCGAG 1037
QY 263 SerLeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGlu 282
Db 1038 TCGGTTCTTATGGCAACGGTCTCACCGAGGATACACCGAGTACGAGTACTACCGTCCC 1097
QY 283 PheAlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMet 302
Db 1098 ATGCGCTGCGGTGACGGCGTTACCCAGCTGTCTTGGACGAGAGCTCTGCGAGTCCATG 1157
QY 303 LysPheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThr 322
Db 1158 GAC-----AACGCTCTTCTCTCGC---TGGCAGCTTATGATGAGTCTTGTACAGTTC 1208
QY 323 AsnArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAsp 342
Db 1209 GAGAGCGCT-----TGGTGTGTCTCCGCGCTCCACTACTGTATAACAAC 1253
QY 343 AsnValGluGlyProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisPro 362
Db 1254 GCCCTCTTGGCCCTTACCAGCGC---ACTGGGAGAAACGCTCTATGATGCTCGTGGTAAG 1310
QY 363 TyrAspAspPro-----ThrProSerTyrTyrAsnLysPheLeuAla 377
Db 1311 TGCAGGATAGCTCTAACCCTTGTCTCTCGCTATGGGCTACGTACGAGGACTACTCTGAAC 1370
QY 378 LysAspSerValMetAspAlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsn 396
Db 1371 AAGCCGAGTATCGAGGCTGTGGCGCTCAGGTCAACGCTACGACTCTGCAACTTT 1430
QY 397 AspValTyrTyrAlaPheGlnGlnThrGlyAspPheValTrpPro-----AsnPheIle 414
Db 1431 GACATCAACCGCAACTTCTCTCCACGCTGACTGGATGAAGCCCTACACCGCTCGTT 1490
QY 415 GluAspLeuGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAsp 433
Db 1491 CCGGACTCTCTGGAG-----CAGATCCCTGTC-----TTGATCTAGCCGCTGAT 1535
QY 434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAsnTrpSer 453
Db 1536 GCTGATTTCAATTCGAACTGCTGGCAACAGGCTCGACTGAAGCCCTGGAGTGGCCC 1595
QY 454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal----- 468
Db 1596 GGACAGGCTGAATATGCTCGCTGAGCTGGAGGATCTGGTCAATTCATGTGCAATGAGCAC 1655
QY 469 AsnGlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyr 488
Db 1656 ACGGCAAGAGATTGGCCAGGTTAAGTCCCATGCAACTTCACCTTCATGCTCTCTAT 1715
QY 489 GluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArg 508
Db 1716 GGTGGTGGCCACATGTTCCCGATGACACCGAGTGGAGTCTCGAGTCTCTCAACCGC 1775
QY 509 ThrIlePheGly---Trp 513

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Db      1776 TGGTTGGAGGTGAATGG 1793
RESULT 11
US-08-967-149-1
; Sequence 1, Application US/08967149
; Patent No. 5939305
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF
; TITLE OF INVENTION: ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59393050 No. 5939305disk of No. 5939305th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,149
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,452
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
; US-08-967-149-1
Alignment Scores:
Pred. No.: 2,79e-54 Length: 2068
Score: 594.00 Matches: 155
Percent Similarity: 46.44% Conservative: 80
Best Local Similarity: 30.63% Mismatches: 174
Query Match: 19.94% Indels: 98
DB: 2 Gaps: 18
US-09-712-338-2 (1-555) x US-08-967-149-1 (1-2068)
QY      45 AlaAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr 64
Db      457 GCCTATGATCTCAGGTGCAAGAACCGATCCCTGCTCTTGGCATC-----GAC 507
QY      65 ProGlyValLysSerTyrSerGlyTyrValValAspThrSerProGlu----- 79

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1431 GACATCAACCGCAACTTCCTCTTCCACGGTGAAGTGAAGAGCCCTACCAACCGCTCTCGTT 1490

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1491 CCGGACTCCTGAG-----CAGATCCCTGTC-----TTGATCTATGCCGGTGAT 1535

434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSer 453

1536 GCTGATTCTATTGCAACTGGCTGGGCAACAAGCGCTGGACTGAAGCCCTGGAGTGGCCC 1595

454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuIysVal----- 468

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469 AsnGlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyr 488

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509 ThrIlePheGly---Trp 513

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RESULT 12

US-09-640-305-3

; Sequence 3, Application US/09640305

; Patent No. RE37447

; GENERAL INFORMATION:

; APPLICANT: Fleer, Reinhard

; Fournier, Alain

; Yeh, Patrice

TITLE OF INVENTION: MODIFIED KLUYVEROMYCES YEASTS, THEIR PREPARATION AND USE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd. 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19002

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/640,305

FILING DATE: 16-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/360,673

FILING DATE: 06-FEB-1995

APPLICATION NUMBER: WO PCT/FR93/00623

FILING DATE: 23-JUN-1993

APPLICATION NUMBER: FR 92/07785

FILING DATE: 25-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Julie K.

REGISTRATION NUMBER: 38 619

REFERENCE/DOCKET NUMBER: ST92040-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)454-3839

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2503 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA


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Db 1188 -----COGGAAGATTGCTTAGATATGAATAGGAATCTACCTCTATGCCTATCG 1235
QY 315 LeuIleSerThrCysLysGlnThrAsnArgThrAlaLeuAlaAspTyrAlaLeuCysAla 334
Db 1236 CTTGTGGACCGCTGTTACAAGTCCCAT-----TCTGTTTCTCTTGTGTG 1280
QY 335 GluAlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyrAlaPheAlaGlyArg 354
Db 1281 TTGGCTGACCGTATTGTGAACAACAGATTACTGGG---GTTTATGAGAAATCAGGTAGG 1337
QY 355 GlyValTyrAspIleArg-----HisProTyrAspAspPro-----Thr 367
Db 1338 AACCTTACGATATTAGATCTAAGTGTGAACGAGGATGATCCGGTGCCTGTATCAG 1397
QY 368 ProProSerTyrTyrAsnLysPheLeuAlaLysAspSerValMetAspAlaIleGlyVal 387
Db 1398 GAAGAAATTTATATCTCTGATTACTTGAATCAGGAGGAAGTTCAAAGAGCTTTAGGAGCT 1457
QY 388 AsnIleAsnTyrThrGlnSer---AsnAsnAspValTyrTyrAlaPheGlnGlnThrGly 406
Db 1458 GATGTGAGTTCTTCCAGGTTGTAGCTCGGATCGGTATCGGTTCGCAATTCACCTGGC 1517
QY 407 AspPheValTrpProAsnPheIleGluAspLeuGluGluIleLeuAlaLeuProValArg 426
Db 1518 GATGGACCGAGCCCA---TTCCACCACTAGCTGCAGAACTTCTTGATCAAGATATCAAT 1574
QY 427 ValSerLeuIleTyrGlyAspAlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaVal 446
Db 1575 GTCTTGATATATGACGCGGATAAGGATATATTGTAATTTGGCTAGGAATCTCGCTGG 1634
QY 447 SerLeuAlaAlaAsnTyrSerGlnAlaAlaGlnPheArgSerAlaGlyTyrTrpProLeu 466
Db 1635 ACTGAAAAATGGAATGGAGGTATACGAAGAGTATATAAAAAACAAGTTTTCAGAACTGG 1694
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Db 1755 TTGAGAATCTATGATGTCGACACATGTTCTCTCAGACCAACCTGAAATTCATTACAA 1814
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RESULT 13
US-08-360-673-3
; Sequence 3, Application US/08360673
; Patent No. 5679544
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: MODIFIED KLUYVEROMYCES YEASTS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,673
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR93/00623
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/07785
; FILING DATE: 25-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST92040-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2503 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Kluyveromyces lactis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 387..1862
; OTHER INFORMATION: /product= "K. lactis protease C
; OTHER INFORMATION: gene"
; OTHER INFORMATION: /gene= "Kl.PRC1"
US-08-360-673-3
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Alignment Scores:
Pred. No.: 2,2e-51 Length: 2503
Score: 568.50 Matches: 151
Percent Similarity: 44.65% Conservative: 66
Best Local Similarity: 31.07% Mismatches: 184
Query Match: 19.08% Indels: 85
DB: 1 Gaps: 14
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US-09-712-338-2 (1-555) x US-08-360-673-3 (1-2503)
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Db 570 GCTTATTCAATGAGAAATTAACCTTTGGATCCCAATCTCTTGGCGTT----- 617
QY 65 ProGlyValLysSerTyrSerGlyTyrValAspThrSerProGluSerHisThrPhePhe 84
Db 618 GATACCGTGAACAATGGTCCGGATATTAGATTACCAGGACTCAAAACACTCTTTTAT 677
QY 85 TrpPheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsnGly 104
Db 678 TGGTTTTTTGAGCTAGAAATGACCAGAGAATGACCCAGTACATATGTTAAACGGT 737
QY 105 GlyProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHisValAsn 124
Db 738 GGTCTGGCTGTCTCTTTCGTGCTCTTCTTTGAATGGGACCTTCTTCTATAGGA 797
QY 125 SerThrPheAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuLeuPhe 144
Db 798 GCTGATTTTGAACCCATTTATTAACCCCTACTCTTGGAAATCCAAAGCTTCTGTATTC 857
QY 145 LeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIleAsn 164
Db 858 CTAGATCAGCCTGTGGTGTGGTCTCTCATACGGTGAC----- 896
QY 165 ProValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrProThr 184
Db 896 ----- 896
QY 185 IleAspAlaThrLeuIleAspThrThrAsnLeuAlaAlaGluAlaAlaTrpGluIleLeu 204
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 Db 1188 -----CCGGAAGATTGCTTAGATATGAATAGGAATCTACCTCTATGCTATCG 1235
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 Db 1236 CTGTGGACCGCTTACACAGTCCAT-----TCTGTTTCTCTGTGTG 1280
 QY 335 GluAlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyrAlaPheAlaGlyArg 354
 Db 1281 TTGCTGACCGTATTGTGGAACAGATTACTGG---GTTTATGAGAATCAGGTAGG 1337
 QY 355 GlyValTyrAspIleArg-----HisProTyrAspPro-----Thr 367
 Db 1338 AACCTTACGATATTAGATCTAAGTGAAGCAGAGGATGATCCGGTGCCTGTTATCAG 1397
 QY 368 ProSerTyrTyrAsnLysPheLeuAlaLysAspSerValMetAspAlaIleGlyVal 387
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 QY 388 AsnIleAsnTyrThrGlnSer---AsnAsnAspValTyrTyrAlaPheGlnThrGly 406
 Db 1458 GATGTGAGTCTTTCCAGAGTGTGAGTTCGGATGTCGGTTCGGATTCAGTGGC 1517
 QY 407 AspPheValTrpProAsnPheIleGluAspLeuGluIleLeuAlaLeuProValArg 426
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 Db 1575 GTCTGTATATGACGCGTAAGGATTAATTTGTAATGGCTAGGAAATCTCGCTGG 1634
 QY 447 SerLeuAlaAlaAsnTyrSerGlnAlaGlnPheArgSerAlaGlyTyrThrProLeu 466
 Db 1635 ACTGAAATTCGATGGAGGTATACGAGAGTATAAAACAAAGTTTTCGAGACTTGG 1694
 QY 467 LysValAsnGlyValGlu-----TyrGlyGluThrArgGluTyrGlyAsnPheSerPhe 484
 Db 1695 AAGAGTGAAGAACACAGATGAGACCAATTCGCGAAACCAATCTTATGGCCCGCTAAC 1754
 QY 485 ThrArgValTyrGluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGln 504
 Db 1755 TTGAAATCTATGATGTCGACATGTTCTCTACGACCACTGAAATTCATTACAA 1814
 QY 505 LeuPheAsnArgThrIle 510
 Db 1815 ATGGTGAATTCATGGATT 1832

RESULT 14

US-08-899-324-32

; Sequence 32, Application US/08899324

; Patent No. 5945329

GENERAL INFORMATION:
 APPLICANT: Breddam, Klaus
 APPLICANT: Keilland-Brandt, Morten
 APPLICANT: Mortensen, Uffe
 APPLICANT: Olesen, Kjeld
 APPLICANT: Stennicke, Henning
 APPLICANT: Wagner, Fred
 TITLE OF INVENTION: CUSTOMIZED PROTEASES
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
 STREET: 3100 No. 5945329west Center, 90 S. 7th Street
 CITY: Minneapolis
 STATE: MN
 COUNTRY: U.S.A.
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/899,324
 FILING DATE: 23-JUL-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/329,892
 FILING DATE: 27-OCT-1994
 APPLICATION NUMBER: 08/144,704
 FILING DATE: 28-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kettleberger, Denise M
 REGISTRATION NUMBER: 33,924
 REFERENCE/DOCKET NUMBER: 8648.44USC1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612/332-5300
 TELEFAX: 612/332-9081
 TELEX:
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2632 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 696..2291
 OTHER INFORMATION:
 US-08-899-324-32

Alignment Scores:
 Pred. No.: 1,81e-46 Length: 2632
 Score: 523.50 Matches: 147
 Percent Similarity: 43.68% Conservative: 74
 Best Local Similarity: 29.05% Mismatches: 200
 Query Match: 17.57% Indels: 85
 DB: 2 Gaps: 19

US-09-712-338-2 (1-555) x US-08-899-324-32 (1-2632)

QY 33 ProLysAsnProThrGlyValIleThr-----LeuThrThrAlaAsnAsn 47
 Db 939 CCAAAATTCCTGAAGCAATCAAAACGAAAGAACTGGGACTTTGTGTCAGAAATGAC 998
 QY 48 ValThrIleArgTyr-----LysGluProGlyAlaGluGlyVal 60
 Db 999 GCAATTTGAAACTATCAGCTTCGTCACAAAGATTAAAGACCTTAAATCTCTGGCATT 1058

QY 61 CysGluThrThrProGlyValIysSerTyrSerGlyTyrValAspThrSerProGlu--- 79
Db 1059 -----GACCAATATGTCACACAGTACCGGTTACTTGGATGTGGAGACGAGAC 1109
QY 80 SerHisThrPhePheThrPheGluAlaArgHisAsnProGluThrAlaProIleThr 99
Db 1110 AAGCATTTCTTCTTTGGACTTTTGAAGTAGAAGCATCTCTGCAAGAGTCCGGTCAATC 1169
QY 100 LeuTrpLeuAsnGlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGly 119
Db 1170 CTTTGGTTGAACGGGGTCCAGGTTGTCTTCACTAACCGGGCTGTCTTTTGAATAGGA 1229
QY 120 ProCysHisValAsnSerThrPheAspAspTyrIleAsnProHisSerTyrAsnGluVal 139
Db 1230 CCCTCATCCATTGGACCTGATTGAACCCCATCGGAACCTTACTCTTGGAAACAGCAAT 1289
QY 140 SerAsnLeuLeuPheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrVal 159
Db 1290 GCCACCGTGATCTCTCTGACACAGCTGTCAACGTTGGTTCGTATTCC----- 1340
QY 160 AspGlySerIleAsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGln 179
Db 1341 -----GGTCCCTCA 1349
QY 180 GlyArgTyrProThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaAlaGluAla 199
Db 1350 GGT-----GTTCCACACTGTCCGCGCTGTAGGAT 1382
QY 200 AlaTrpGluIleLeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGln 219
Db 1383 GTCTATAACTTCTTGGAGTTGTTCTTCGATCAGTTCCTCAATAGCGTCAACAGGGCCAA 1442
QY 220 SerIysAspPheSerLeuTrpThrGluSerTyrGlyHisTyrGlyProAlaPhePhe 239
Db 1443 -----GATTTCCATCTCGTGGGAATCTACCGCGCATTTACATCCCTGTTTGGC 1496
QY 240 AsnHisPheTyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeu 259
Db 1497 TCTGAAATTTGTTCTCACAAGGACAG----- 1523
QY 260 AsnPheAsnSerLeuGlyIleIle-----AsnGlyIleIleAspGluAlaIleGlnAla 277
Db 1524 AACTTCAACTTAACCTCCGCTTGTGCGAATGGCTCACTGACCCATTGACTCAGTAT 1583
QY 278 ProTyrTyrProGluPheAlaValAsnAsnThrTyrGlyIleIysAlaValAsnGluThr 297
Db 1584 AACTATTACCAACCAATGGCCTGTGTGAAGGT---GGCGAACCATCTGTT----- 1631
QY 298 ValTyrAsnTyrMetIysPheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSer 317
Db 1632 -----TTGCCCTCGGAGGATGCTCTGCTATGGAAGACTCTTTGGAA 1673
QY 318 ThrCysGlnThrAsnArgThrAlaLeuAlaAspTyrAlaLeu-----CysAlaGlu 335
Db 1674 CGTTGTTGGCTTGTATCGAGTCTGCTATGACTCGCAATCGCTGCTGCTGTGTTCCA 1733
QY 336 AlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyrAlaPheAlaGlyArgGly 355
Db 1734 GCTACCATTTATTGTAATAACGCCCAATTTGGCTCTTACCAAGT---ACCGGCAGAAAC 1790
QY 356 ValTyrAspIleArgHisProTyrAspAsp-----ProThrProProSer 370
Db 1791 GTTTACGATACAGGAAGGATTGTGAAGTGGCAATTTGTGCTACCAAGTTACAGAT 1850
QY 371 TyrTyrAsnLysPheLeuAlaLysAspSerValMetAspAlaIleGlyValAsnIleAsn 390
Db 1851 ---ATCGACGACTACTTAAACACGAGTACGTCAAGAGAGCTGTCGTCGGAGGTTGAC 1907
QY 391 TyrThrGlnSer---AsnAsnAspValTyrTyrAlaPheGlnGlnThrGlyAspPheVal 409
Db 1908 CACTAGAAATCTGTAACTTCGATATCAACAGAAATTTCTGTTTTCGGGTGATTGGATG 1967
QY 410 TrpProAsnPheIleGluAspLeuGluIleLeuAlaLeuProValArgValSerLeu 429

Db 1968 AAGCCT---TACCACACCGCCGTAACAGATCTTTTGAATCAAGACCTTACCATTCTGGTA 2024
QY 430 IleTyrGlyAspAlaAspTyrIleCysAsnTyrPheGlyGlyGlnAlaValSerLeuAla 449
Db 2025 TATGACGGCGATAAAGATTTCATCTGTAACCTGTTGGTAAATAGGGGTGACCGATGTC 2084
QY 450 AlaAsnTyrSerGlnAlaAlaGlnPheArgSer-----AlaGlyTyrThrProLeu 466
Db 2085 TTGCCATGGAAGTACGACGAGAAATTTGCAAGCAAAAGTACGTAACTGACTGCTTCT 2144
QY 467 LysValAsnGlyValGluTyrGlyThrArgGluTyrGlyAsnPheSerPheThrArg 486
Db 2145 ATCACCAGCAGAGTCGCT---GGTGAAGTCAATCTTACAGCACCTTACCTATTGAGA 2201
QY 487 ValTyrGluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPhe 506
Db 2202 GTCTTCAATGGTGGCCACATGGTTCATTTGACGTCCCTGAAACCGCTTAAGTATGTT 2261
QY 507 AsnArgThrIlePheGly 512
Db 2262 AACGAATGGATCCACGGT 2279
RESULT 15
US-08-329-892B-32
; Sequence 32, Application US/08329892B
; Patent No. 6187579
; GENERAL INFORMATION:
; APPLICANT: Breddam, Klaus
; APPLICANT: Kelland-Brandt, Morten
; APPLICANT: Mortensen, Uffe
; APPLICANT: Olesen, Kjeld
; APPLICANT: Stennicke, Henning
; APPLICANT: Wagner, Fred
; TITLE OF INVENTION: CUSTOMIZED PROTEASE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6187579west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,892B
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/144,704
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettleberger, Denise M
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 8648.44US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:

ORIGINAL SOURCE:

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 696...2291

; OTHER INFORMATION:

US-08-329-892B-32

Alignment Scores:

Pred. No.:	1.81e-46	Length:	2632
Score:	523.50	Matches:	147
Percent Similarity:	43.68%	Conservative:	74
Best Local Similarity:	29.05%	Mismatches:	200
Query Match:	17.57%	Indels:	85
DB:	3	Gaps:	19

US-09-712-338-2 (1-555) x US-08-329-892B-32 (1-2632)

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Qy 33 ProLysAsnProThrGlyValLysThr-----LeuThrThrAlaAsnAsn 47
Db 939 CCAAAATTCCTGAAGCAATCAAAACGAAGAAGACTGGGACTTTGTGTCAGAAATGAC 998
Qy 48 ValThrIleArgTyr-----LysGluProGlyAlaGluGlyVal 60
Db 999 GCAATTGAAAACATATCAGCTTCGTGTCAACAGATTAAAGGACCCCTAAATAATCCTGGGCAT 1058
Qy 61 CysGluThrThrProGlyValLysSerTyrSerGlyTyrValAspThrSerProGlu--- 79
Db 1059 -----GACCCAAATGTACACAGTACACGGGTACTTGGATGTGGAAAGACGAGGAC 1109
Qy 80 SerHisThrPhePheThrPheGluAlaArgHisAsnProGluThrAlaProIleThr 99
Db 1110 AAGCATTTCTTTTGGACTTTTGAAGTAGAAGACGATCCTGCAAGGATCCGGTCA 1169
Qy 100 LeuTrpLeuAsnGlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGly 119
Db 1170 CTTTGGTTGAACGGGGTCCAGGTTGTTCTTCACTAAACCGGGCTGTTCTTTGAATTAGGA 1229
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Db 1230 CCTCATCATCTGGACCTGATTTGAAACCCATCGGGAACCTTACTCTTGAACAGCAAT 1289
Qy 140 SerAsnLeuLeuPheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrVal 159
Db 1290 GCCACCGGATCTTCTTGACCGAGCTGTCAACGTTGGGTTCTCGTATTTC----- 1340
Qy 160 AspGlySerIleAsnProValThrGlyValValGluAsnSerSerPheAlaGlyValGln 179
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Qy 200 AlaTrpGluIleLeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGln 219
Db 1383 GTCATATACTTCTTGAGTGTGTTCTTCGATCAGTTCCTGATACGTCAACAAGGGCCAA 1442
Qy 220 SerLysAspPheSerLeuThrThrGluSerTyrGlyHisTyrGlyProAlaPhePhe 239
Db 1443 -----GATTTCCACATCGCTGGGAATCCTACGCGCGCCATTATCATCCCTGTTTTCGCC 1496
Qy 240 AsnHisPheTyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeu 259
Db 1497 TCTGAAATTTGTCTCAACAGGACAGA----- 1523
Qy 260 AsnPheAsnSerLeuGlyIleIle-----AsnGlyIleIleAspGluAlaIleGlnAla 277
Db 1524 AACTTCAACTTAACCTCCGCTGTGATCGGAATAGCCCTCAGTACCCATTGACTCAGTAT 1583
Qy 278 ProTyrTyrProGluPheAlaValAsnAsnThrTyrGlyIleLysAlaValAsnGluThr 297
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Qy 298 ValTyrAsnTyrMetLysPheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSer 317
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Qy 318 ThrCysLysGlnThrAsnArgThrAlaLeuAlaAspTyrAlaLeu-----CysAlaGlu 335
Db 1674 CGTTGTTTGGGCTTGATCGAGTCGTCGTATGACTCGCAATCGGTCTCGTCTGTTGCCA 1733
Qy 336 AlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyrAlaPheAlaGlyArgGly 355
Db 1734 GCTACCAATTATTGTAATAACGCCCAATTTGGCTCTTACCACGT-----ACGGCAGAAAC 1790
Qy 356 ValTyrAspIleArgHisProTyrAspAsp-----ProThrProProSer 370
Db 1791 GTTTACCATATCAGGAAGGATTGTGAAGGTGGCAATTTGTGCTACCCCAACGTTCAAGAT 1850
Qy 371 TyrTyrAsnLysPheLeuAlaLysAspSerValMetAspAlaIleGlyValAsnIleAsn 390
Db 1851 ---ATCGACGACTACTTAAACACGAGACTACGTCAAAGAAGCTGTGGTGGGAGGTTGAC 1907
Qy 391 TyrThrGlnSer---AsnAsnAspValTyrTyrAlaPheGlnGlnThrGlyAspPheVal 409
Db 1908 CACTACGAATCCTGTAACTTCGATATCAACAGAAATTTCTGTTTGGGATGATGGATG 1967
Qy 410 TrpProAsnPheIleGluAspLeuGluGluIleLeuAlaLeuProValArgValSerLeu 429
Db 1968 AAGCT---TACCACACCGCGTAAACAGATCTTTTGAATCAAGACCTTACCCATTTGTA 2024
Qy 430 IleTyrGlyAspAlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAla 449
Db 2025 TATGACGGCGATAAAGATTTTCATCTGTAAGTGGTAAATAAGGCGTGGACGGATGTC 2084
Qy 450 AlaAsnTyrSerGlnAlaAlaGlnPheArgSer-----AlaGlyTyrThrProLeu 466
Db 2085 TTGCCATGGAAGTACGAGGAAGATTTGCAAGCCCAAAAGTACGTAAGTGGACTGCTTCT 2144
Qy 467 LysValAsnGlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArg 486
Db 2145 ATCACCAGCAGAGGTGCGCT---GGTGAAGTCAATCCTACAAGCACTTCACCTATTGAGA 2201
Qy 487 ValTyrGluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPhe 506
Db 2202 GTCTTCAATGTTGGCCACATGGTTCCATTTCAGCTCCCTGAAACGCGCTTAAGTATGTT 2261
Qy 507 AsnArgThrIlePheGly 512
Db 2262 AACGAATGGATCCACGGT 2279

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Search completed: July 29, 2004, 13:38:07

Job time : 133 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 29, 2004, 11:31:29 ; Search time 702 Seconds
(without alignments)
3876.414 Million cell updates/sec

Title: US-09-712-338-2
Perfect score: 2979
Sequence: 1 MRGYEFLVSLPLVAASWALP.....HTQSSVPLTATSSSSVGMA 555

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications_NA -QFMT=fastap -SUFFIX=rnnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -START=1 -END=-1 -MATRIX=blomsu62
-TRANS=human40.cdi -LIST=45 -DOALIGN=15 -MODE=LOCAL -OUTFMT=ptc -THR SCORE=pct -THR MAX=100
-NCPU=6 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -THR SCORE=pct -THR MAX=100
-MAXLEN=200000000 -USERS=US09712338 @CGN 1.1 2.21 @runat_22072004_170322_10413
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
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- 19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
SUMMARIES					
*					

ALIGNMENTS

RESULT 1

US-10-369-493-36581
; Sequence 36581, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36581
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-369-493-36581

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2	812.5	27.3	1686	16	US-10-369-493-27042	Sequence 27042, A
3	636	21.3	1527	16	US-10-369-493-25156	Sequence 25156, A
4	588.5	19.8	2218	15	US-09-993-192-1	Sequence 1, Appli
5	588.5	19.8	2218	15	US-10-206-619-1	Sequence 1, Appli
6	539	18.1	1289	16	US-10-369-493-3620	Sequence 3620, A
7	530.5	17.8	1619	16	US-10-369-493-27598	Sequence 27598, A
8	527.5	17.7	1599	16	US-10-369-493-25613	Sequence 25613, A
9	479.5	16.1	1751	13	US-10-425-114-6406	Sequence 6406, Ap
10	475	15.9	1551	9	US-09-938-842A-683	Sequence 683, App
11	475	15.9	1551	11	US-09-938-842A-683	Sequence 683, App
12	473	15.9	1855	13	US-10-425-114-11176	Sequence 11176, A
13	468.5	15.7	2018	17	US-10-437-963-52572	Sequence 52572, A
14	464.5	15.6	1768	16	US-10-382-239A-1	Sequence 1, Appli
15	463	15.5	1913	13	US-10-424-599-59411	Sequence 59411, A
16	455	15.3	1755	17	US-10-437-963-53563	Sequence 53563, A
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19	397.5	13.3	1696	17	US-10-437-963-57156	Sequence 57156, A
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21	382	12.8	1326	13	US-10-425-114-27988	Sequence 27988, A
22	381.5	12.8	1326	13	US-10-425-114-27988	Sequence 27988, A
23	375.5	12.6	1503	17	US-10-437-963-97753	Sequence 97753, A
24	372	12.5	1886	13	US-10-424-599-26173	Sequence 26173, A
25	368.5	12.4	1514	13	US-10-425-114-29826	Sequence 29826, A
26	368	12.4	1890	13	US-10-425-114-26356	Sequence 26356, A
27	366.5	12.3	1949	10	US-09-971-429B-33	Sequence 33, Appli
28	361	12.1	1551	14	US-10-084-018-4	Sequence 4, Appli
29	360	12.1	2100	13	US-10-424-599-139251	Sequence 139251, A
30	359	12.1	1697	10	US-09-796-753-39	Sequence 39, Appli
31	359	12.1	1963	13	US-10-296-115-586	Sequence 586, App
32	359	12.1	2076	9	US-09-909-320-163	Sequence 163, App
33	359	12.1	2076	9	US-09-909-088B-163	Sequence 163, App
34	359	12.1	2076	9	US-09-905-291A-163	Sequence 163, App
35	359	12.1	2076	9	US-09-902-853-163	Sequence 163, App
36	359	12.1	2076	9	US-09-907-824-163	Sequence 163, App
37	359	12.1	2076	9	US-09-907-841-163	Sequence 163, App
38	359	12.1	2076	10	US-09-904-011-163	Sequence 163, App
39	359	12.1	2076	10	US-09-906-742-163	Sequence 163, App
40	359	12.1	2076	10	US-09-906-838-163	Sequence 163, App
41	359	12.1	2076	10	US-09-907-613-163	Sequence 163, App
42	359	12.1	2076	10	US-09-907-942-163	Sequence 163, App
43	359	12.1	2076	10	US-09-904-859-163	Sequence 163, App
44	359	12.1	2076	10	US-09-909-204-163	Sequence 163, App
45	359	12.1	2076	10	US-09-904-820-163	Sequence 163, App

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 Query Match: 63.18% Indels: 133
 DB: 16 Gaps: 8

US-09-712-338-2 (1-555) x US-10-369-493-36581 (1-1859)

QY 26 SerValGlyArgArgGlnLeuProLysAsnProThrGlyValLysThrLeuThrAla 45
 DB 19 TCITTTCAACAGCAGCAGCTACCGAGCCCAACTGGTGTCAAGAAATCAACAGCTCCC 78
 QY 46 AsnAsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrPro 65
 DB 79 AATGGTGTGACCATCCGATACAGAGAGCCTGGTAAAGAGGGGTGTCTGTGAGACGACCCCT 138
 QY 66 GlyValLysSerTyrSerGlyTyrValAspThrSerProGluSerHisThrPhePheTrp 85
 DB 139 GGTGTCAACTCTTACTCTGGATAGCTGTATCTATCGCTGAGTCTCACACCTCTCTTTTAC 198
 QY 86 PhePheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsnGlyGly 105
 DB 199 TTTCTTGAAGCTCGTCATGACCCGCGCAACGCTCTATCACTCTGTGGCTGAATGGTGGC 258
 QY 106 ProGlySerAspSerLeuIleGlyLeuPheGlu 116
 DB 259 CCCGGAAGTGATTCGCTTATCGGGCTTTTGA-AGGTTGTACTGCTGACTGGGTACA 317
 QY 117 -----GluLeuGlyProCysHisValAsnSerThr 126
 DB 318 AGAAGTTGATGACTGATGGGCTTCTTGTAGAACTGGGACCGTGGCTATCAGCGAGAAC 377
 QY 127 PheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuPheLeuSer 146
 DB 378 CTGAGCAGCTAGTCAACCCATACCTACTCGTGGATGAAGTCTCAACCTTTGTTCATCTCG 437
 QY 147 GlnProLeuGlyVal 151
 DB 438 CAGCCATTGGGAGTCGGTATGAAGAAATGTGTCTTTAGTCTGTCGAGCTTCTCACTG 497
 QY 152 -----GlyPheSerTyrSerAspThrValAspGlySerIleAsnProValThrGlyVa 169
 DB 498 GSCCATAGGATTTCTGATCGGAAACACAGAGAGGGTGGCTCAATCCCGTCCCGGGT 557
 QY 169 lValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrProThrIleAspAlaThrLe 189
 DB 558 GGTGAGGATAGTTCTTTGCTGGGTCCAGGTCGCTATCCCAAAATCAACGCTACCT 617
 QY 189 ule-----As 191
 DB 618 GAC-CGGTAATTTCTCAACAAACGTCGATGCTCTAGTTTATAGAGCTAAAGCTGTACTAGA 676
 QY 191 pThrThrAsnLeuAlaAlaGluAlaAlaTrpGluIleLeuGlnGlyPheLeuSerGlyLe 211
 DB 677 TACCAACCGAGCTCGCGGAGGCACTTTGGGAAAGTCGTGAGGGGCTTTCTCGGTGGT 736
 QY 211 uProSerLeuAspSerArgValGlnSerLysAspPheSerLeuTrpThrGluSerTyrGl 231
 DB 737 ACCTCAGTTGGACAGCACTATCAAGTCCAAAGACTTAAATTTATGAGCTGAGAGTTACGG 796
 QY 231 YGlyHisTyrGlyProAlaPhePheAsnHisPheTyrGluGlnAsnGluArgIleAlaAs 251
 DB 797 AGGACACTACGGTCCCGCATCTTCTCAATCACTTTTACGAGCAGAACCAAAAAATTCGCAA 856
 QY 251 nglySerValAsnGlyValGlnLeuAsnPheAsnSerLeuGlyIleIleAsnGlyIle1 271
 DB 857 CGGAACCATGTGATGGTATGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 916
 QY 271 eAspGluAlaIleGln----- 276

DB 917 CGATGAGGGGATTCAGGTACGGGATACAAAGCGCTCAGCAATATCTCTCTGACTAGAA 976
 QY 277 -----AlaProTyrTyrProGluPheAlaValAsnAsnThrTyrGlyIleAlaAala 293
 DB 977 ACTAGGCACTTTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 1035
 QY 294 -----ValAsnGluT 297
 DB 1036 AGTACTGTCTTTTTCAGCAAAATGGACGACATACTTACAAGCTGAAAAACAGGTTAAACGAGA 1095
 QY 297 hrValTyrAsnTyrMetLysPheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleS 317
 DB 1096 CAGTCTACAACTACATGAAATTTGCCAACAGATGGCAACCGGATGCCGATCAGATTG 1155
 QY 317 erThrCysLysGlnThrAsnArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaT 337
 DB 1156 CCCTCTCAAGCAACAAACCGTCTCTTTTGGCGACTATGCTCTCTGCTCGAGGCGAA 1215
 QY 337 hrAsnMetCysArgAspAsnValGluGlyProTyrTyr----- 349
 DB 1216 CTAACATGTGCAGAGATAACGTT---GGTACGTACTTCTACCTGAGACTCTGGGAAAGTA 1272
 QY 350 -----AlaPheAlaGlyArgGlyV 356
 DB 1273 ATCAGCTGATTTATCTTCCACAGAGGACTCTCTACTACAGGCTACGA-GCAACTCGAGGCG 1331
 QY 356 alTyrAspIleArgHisProTyrAsp----- 364
 DB 1332 TATATGATTCATTCGCGCCCGCACAAATGTAGCCGCTGATCCTAATCCAGGTTCTCTATAC 1391
 QY 365 -----AspProThrProProSerTyrTyrAsnLysPheLeuAlaLysAsps 380
 DB 1392 TAAATAGGAAAGAGCCCAACACCCCGAACCTCTTCGCTCCCTTCTCCAGCAAGACT 1451
 QY 380 erValMetAspAla-IleGlyValAsnIleAsnTyrThrGlnSerAsnAspValTyr 399
 DB 1452 GGGTCATGATGCTTCTTGGCGTGAACATCAACTACACCTCTTCCAAATAACGAAATTTAC 1511
 QY 400 TyrAlaPheGlnThrThrGlyAspPheValTrpProAsnPheIleGluAspLeuGluGlu 419
 DB 1512 TATGCTTTCAGCAAAACCGGTGATTTCTTTTGGCCCACTTCACTCAGGATCTCGAGAA 1571
 QY 420 IleLeuAlaLeuProValArgValSerLeuIleTyrGlyAspAlaAspTyrIleCysAsn 439
 DB 1572 ATCTCTACCTACCCAGTCCGCTCAGTCTGATCTATGCGCAGCAGACTACATCTGCAAC 1631
 QY 440 TrpPheGlyGlyGlnAlaValSerLeuAlaAsnTyrSerGlnAlaAlaGlnPheArg 459
 DB 1632 TGGTTGCGAGGCCAAGCGCTCTCCCTCGCGTCAAGTACCCGCAATCCCAAGCAGTCCAG 1691
 QY 460 SerAlaGlyTyrThrProLeuLysValAsnGlyValGluTyrGlyThrArgGluTyr 479
 DB 1692 GCCCGCGGATACACGCTTCTTGTGATGGGTGGAGTACGGAGAGACTCGAGATAT 1751
 QY 480 GlyAsnPheSerPheThrArgValTyrGluAlaGlyHisGluValProTyrTyrGlnPro 499
 DB 1752 GGCATTTCTCTCTCCGCTGCTATGAGCGCGCCACGAGGTTCTTACTATCAGCT 1811
 QY 500 IleAlaSerLeuGlnPheAsnArgThrIlePheGlyTrpAspIle 515
 DB 1812 GCTGCGTCTGCTGAGCTTTTAAACCGCACTTTTGTGGTGGGATATT 1859

RESULT 2

US-10-369-493-27042
 ; Sequence 27042, Application US/10369493
 ; Publication NO. US2003023675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

33	ProLys	AsnProThrGlyValLysThrLeuThrThrAlaAsn-----AsnValThrIle	50
82	CCATATCAAGCTGTGGCTTGAAGACAGTCACTTCCACACCGCAACATCAAGATC	141	
51	ArgTyrLysGluProGlyAlaGluGlyValCysGluThrThr---ProGlyValLysSer	69	
142	TCGTACAAGAACCC-----AAGGATGTCGTGACGACTGCTTTCACAGCGCAGACGAG	195	
70	TyrSerGlyTyrValAspThrSerProGlu-----SerHisThrPhePheThrPhePhe	87	
196	TACACCGGCTGGTTCACGTCGCCGGCAGATACCCACACACACTCTCTCTCTGCTGTGT	255	
88	GluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsnGlyGlyProGly	107	
256	GGTGCCCGCGAG-----CCAACCTCTCGCTGACAATGATGCTCAACGGCGGGCCCGGC	309	
108	SerAspSerLeuLeGlyLeuPheGluGluLeuGlyProCysHisVal-----	123	
310	TCGAGTTCATGCTTTGGCCTGTCGCCGAGAATGGCCCTTGCAGGTCGTCGAGAGAGGC	369	
124	AsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuLeu	143	
370	GCCAGCCGCCCTGGAGACGGCCGCCAGAGAAATGGGGCTGGGATAGAGCTCCCATATGTC	429	
144	PheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIle	163	
430	TTTGTGCACAGCCCAACCATGTGCGTTTCTCATACGATACTCCCAACCAACGGTTCTCTG	489	
164	AsnProValThrGlyValValGlu-----	171	
490	GACTTGACGACTGGATGGTGTGCCTACCATGCAATGGCTGATAACTGCTGCCACGC	549	
172	-----AsnSerSerPheAla-----GlyValGlnGlyArgTyrProThrIleAsp	186	
550	CTCTTCTCAACGCGCAGGTTTCTCTCAAAACAACATCCAA-----	588	
187	AlaThrLeuIleAspThrThrAsnLeuAlaGluAlaAlaTrpGluLeuLeuGlnGly	206	
589	---AACAGGCCAACACGACTCAGAATGCTGCCATGCGCGCTCTACCCACTGCTCCAGGGG	645	
207	PheLeuSerGlyLeuProSer---LeuAspSerArgValGlnSerIlyAspPheSerLeu	225	
646	TTCTGTAGTACTTCCCGGAGTAGCTCCCGGACAAGCAGCCGCTGGCGCGTAAACCTC	705	
226	TrpThrGluSerTyrGlyHisTyrGlyProAlaPhePheAsnHisPheTyrGluGln	245	
706	TTTACGGAAGATTATGCGCGCCACTACGGGCGCTGTCTTTCCGCGACACCTGGCAGAGGAG	765	
246	AsnGluArgIleAlaAsnGlySerVal-----AsnGly	256	

;; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

;; FILE REFERENCE: 38-10(52052)B

;; CURRENT APPLICATION NUMBER: US/10/369,493

;; CURRENT FILING DATE: 2003-02-28

;; PRIOR APPLICATION NUMBER: US 60/360,039

;; PRIOR FILING DATE: 2002-02-21

;; NUMBER OF SEQ ID NOS: 47374

;; SEQ ID NO 25156

;; LENGTH: 1527

;; TYPE: DNA

;; ORGANISM: Saccharomyces cerevisiae

US-10-369-493-25156

Alignment Scores:

Pred. No.: 1.87e-65 Length: 1527
Score: 636.00 Matches: 167
Percent Similarity: 46.29% Conservative: 70
Best Local Similarity: 32.62% Mismatches: 197
Query Match: 21.35% Indels: 78
DB: 16 Gaps: 14

US-09-712-338-2 (1-555) x US-10-369-493-25156 (1-1527)

QY 19 LeuProGlySerThrProAlaSerValGlyArgArgGlnLeu-----ProLys 34
DB 127 CTTCACAGAAACACAGCAACCCCTTAANTGGACCGTTGAATCAGCATCCGCTG 186
QY 35 AsnProThrGlyValLeuThrThrAlaAsnAsnValThrIleArgTyrLysGlu 54
DB 187 TTTACAACTTTTATCTCTCTGGACACAGATTACAGTTTGAGACTTTAGAACATAGAT 246
QY 55 ProGlyAlaGluGlyValCysGluThrThrProGlyValLysSerTyrSerGlyTyrVal 74
DB 247 CCTCTAACTAGGAATT-----GACACCGTAAACAAATGGTGGGTACATG 294
QY 75 AspThrSerProGluSerHisThrPheThrPhePheGluAlaArgHisAsnProGlu 94
DB 295 GACTATAGGATTCACAAACACTTTTCTACTGGTTTGTGAAGTAGGACGATCCTGCT 354
QY 95 ThrAlaProIleThrLeuTrpLeuAsnGlyGlyProGlySerAspSerLeuIleGlyLeu 114
DB 355 AACGACCCAAATATTCTTTGGTTAAATGGTGACCTGTTGTCTCTGTTTACTGGTGTG 414
QY 115 PheGluGluLeuGlyProCysHisValAsnSerThrPheAspTyrIleAsnProHis 134
DB 415 CTATTGGAATAGAGCCCTCATCAATTTGGCGCGATATGAAACCAATCCATCCCTAT 474
QY 135 SerTrpAsnGluValSerAsnLeuLeuPheLeuSerGlnProLeuGlyValGlyPheSer 154
DB 475 TCTTGGAAATAAACGCTTCAATGATCTTCTTAGAACACCCACTCGAGTCGGCTTTTCC 534
QY 155 TyrSerAspThrValAspGlySerIleAsnProValThrGlyValValGluAsnSerSer 174
DB 535 TATGGTGTAT----- 543
QY 175 PheAlaGlyValGlnGlyArgTyrProThrIleAspAlaThrLeuIleAspThrThrAsn 194
DB 544 -----GAAAGTCTCTCTACAAA 564
QY 195 LeuAlaAlaGluAlaAlaTrpGluIleLeuGlnGlyPheLeuSerGlyLeuProSerLeu 214
DB 565 TTAGCAGGCAAGATCGGTACATTTTCTCTGGAATTTGTTTGAAGCTTTCTCTCATTTA 624
QY 215 AspSerArgValGlnSerLysAspPheSerLeuThrThrGluSerTyrGlyGlyHisTyr 234
DB 625 -----CGCTCCACAGATTTCACATTCAGCGGCAATCCCTATCGAGCACTATAT 672
QY 235 GlyProAlaPhePheAsnHisThrTyrGluGlnAsn---GluArgIleAlaAsnGlySer 253
DB 673 ATCCCTCAAAATTCACATGAGATCGTTGTCAAGAACCTGGAAGA----- 717
QY 254 ValAsnGlyValGlnLeuAsnPheAsnSerLeuGlyIleIleAsnGlyIleIleAspGlu 273

DB 718 -----ACGTTCAATTTAACTTCAGTTATGATTGTAATGGTATCAGACACCT 765
QY 274 AlaIleGlnAlaProTyrTyrProGluPheAlaVal---AsnAsnThrTyrGlyIleLys 292
DB 766 TTGATTCAAGCAGATTATTATGAACCAATGGCATCGCGGAAAGGGGCTATCACCTGTT 825
QY 293 AlaValAsnGluThrValTyrAsnTyrMetLysPheAlaAsnGlnMetProAsnGlyCys 312
DB 826 CTCTCATCAGAGAAATCGAGAAATAGTAAAGCTGCAGTCTCT----- 870
QY 313 GlnAspLeuIleSerThrCysLysGlnThrAsnArgThrAlaLeuAlaAspTyrAlaLeu 332
DB 871 -----TGTCTAGGTGTGAACAAGTTATGTTATGCTTCTAAATCAAGT 912
QY 333 -----CysAlaGluAlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyrAla 350
DB 913 TTACATGATCATGTCGCCACTGCTTACTGTGACTCTGCACCTTTTGGAAACCGTACATTAA 972
QY 351 PheAlaGlyArgGlyValTyrAspIleArgHisProTyrAspAspPro----- 366
DB 973 ---ACAGGACTCAACGCTCATGACATTAGAGGGCCCTGTGAAGATATAATAGTACTGATGGT 1029
QY 367 -----ThrProSerTyrTyrAsnLysPheLeuAlaLysAspSerValMetAsp 383
DB 1030 ATGTGTTATACAGGTCTCCGCTATGTCGACCATATATGAATTTTCTGAAAGTTCAAGAA 1089
QY 384 AlaIleGlyValAsnIle---AsnTyrThrGlnSerAsnAsnAspValTyrTyrAlaPhe 402
DB 1090 AGCTTAGGTCTCGAGTCGATTAATTTCTGCTGTGTATGATGACGTGTTCAACCGATTT 1149
QY 403 GlnGlnThrGlyAspPheValTrpAsnPheIleGluAspLeuGluGluLeuAla 422
DB 1150 TTGTTTACGGCGGATGAAGTAAACCA---TTTCAACAATATATATGCTGAATTTAATAA 1206
QY 423 LeuProValArgValSerLeuIleTyrGlyAspAlaAspTyrIleCysAsnTrpPheGly 442
DB 1207 CACAACATCCGGTATTAAATATATGCGGTGATAGGATTATTTGTAATTTGGTGGGA 1266
QY 443 GlyGlnAlaValSerLeuAlaAsnTyrSerGlnAlaAlaGlnPheArgSerAlaGly 462
DB 1267 AACCATGCTTGTCCAAATGAGTTGGAATGGATCAATAACGTAGTATCAGAGAAGATG 1326
QY 463 TyrThrPro-----LeuLysValAsnGlyValGluTyrGlyThrArgGluTyrGly 480
DB 1327 TTAAGACCATGGTCAAGTAAAGAAACAGGTGAAGAGTTGGGACAAAGTCAAGAACTATGC 1386
QY 481 AsnPheSerPheThrArgValTyrGluAlaGlyHisGluValProTyrTyrGlnProIle 500
DB 1387 CTTTTACCTTTTGGAGAAATATACGATCCGCTCATATGGTCCCTATGATCAACCGGAG 1446
QY 501 AlaSerLeuGlnLeuPheAsnArgThrIlePheGly 512
DB 1447 GCAGTTTGAATAAGTCAACAGTTGGATTTCGGT 1482

RESULT 4

US-09-993-192-1

; Sequence 1, Application US/09993192

; Publication No. US20020150983A1

; GENERAL INFORMATION:

; APPLICANT: Korea Research Institute of Bioscience and Biotechnology

; APPLICANT: Dong Kook Pharmaceutical Co.

; APPLICANT: Rhee, Sangki

; APPLICANT: Choi, Hui-sung

; APPLICANT: Kang, Hyunah

; APPLICANT: Sohn, Junghoon

; APPLICANT: Bae, Junghoon

; APPLICANT: Kim, Moowoon

; APPLICANT: Agaphonov, Michasel

; TITLE OF INVENTION: Hanesula polymorpha mutants and process for the preparation of

; FILE REFERENCE: 4220-116 US

; CURRENT APPLICATION NUMBER: US/09/993,192

; CURRENT FILING DATE: 2001-11-14


```

; APPLICANT: Kim, Moowoon
; APPLICANT: Agapshonov, Michael
; TITLE OF INVENTION: Hansenula polymorpha mutants and process for the preparation of
; TITLE OF INVENTION: recombinant proteins using the same
; FILE REFERENCE: 4220-116 US
; CURRENT APPLICATION NUMBER: US/10/206,619
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US/09/674,617
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: PCT/KR00/00173
; PRIOR FILING DATE: 2000-03-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2218
; TYPE: DNA
; ORGANISM: Hansenula polymorpha DL1
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U67174
; DATABASE ENTRY DATE: 1996-08-17
; RELEVANT RESIDUES: (1)..(2218)
US-10-206-619-1

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QY	210	GlyLeuProSerLeuAspSerArgValGlnSerLysAspPheSerLeuThrThrGluSer	229
DB	1137	CAATTCCCAACACCTT-----CTGAAGAACGACTTCCACATCCCGCGGAGTCG	1184
QY	230	TyrGlyGlyHisTyrGlyProAlaPhePheAsnHisPheTyrGluGlnAsnGluArgIle	249
DB	1185	TACGGTGGTCATTACATCCAGTGTTCCTCCGAGATTCTCACCCATCGTACAGAA---	1241
QY	250	AlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSerLeuGlyIlelleAsnGly	269
DB	1242	-----TCTTTCAACCTCAGTTCGGTGTGATTGGTAAACGGT	1277
QY	270	IleIleAspGluAlaIleGlnAlaProTyrTyrProGluPheAlaValAsnAsnThrTyr	289
DB	1278	TTGACGACCCACTTAACAGTAGCCATCTACAGAGAATGGCATGCTCTACTGATGTT	1337
QY	290	GlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLysPheAlaAsnGlnMetPro	309
DB	1338	GGCTATGAGCAA---CCCTGACGAGCTCTGAGTGCAGGAAGAAATGTTTGGAGACCTTGCCT	1394
QY	310	AsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsnArgThrAlaLeuAlaAsp	329
DB	1395	AGA---TGTTGTGATTGATTGAATCATGCTACAGCTCGAG-----TCT	1436
QY	330	TyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyr	349
DB	1437	GTGTTCTCATGTGTCGCGGCTCCACTACTGTCACAAACACGACCACTTGACCATTC	1496
QY	350	AlaPheAlaGlyArgGlyValTyrAspIleArgHisPro-----Tyr	363
DB	1497	AAG---ACCGGCAGAAACGCTACGAGCTTAGAAAGATGTCGAGGAACTCTGTGCTAC	1553
QY	364	AspAspProThrProProSerTyrTyrAsnLysPheLeuAlaLysAspSerValMetAsp	383
DB	1554	AAAGAC-----ATGGAATCATTTGACCAATATTTGACACGAGACTTTGTCAAGGAA	1604
QY	384	AlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsnAspValTyrTyrAlaPhe	402
DB	1605	AAGTTGGCGCTGAGGTTGACACTTACGAGTCGTGTAATTTTCGACGTGAACAGAACTTC	1664
QY	403	GlnGlnThrGlyAspPheValTyrPro-----AsnPheIleGluAspLeuGluGlu	419
DB	1665	CTGTTTCTGGTGTGATGGATGAACCTTACCAAGAACCTTATCAATCTCTGGAGCAA	1724
QY	420	IleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAspAlaAspTyrIleCys	438
DB	1725	-----GGTCTTCTGTC-----CTGATTTACGACGAGACCAAGGATTTTCATCTGC	1769
QY	439	AsnTrpPheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSerGlnAlaAlaGlnPhe	458
DB	1770	AATTGGCTCGGAACCAAGCGCTGGTCCCAATGAGCTCCCTTGGTCTGGACACGATGAATC	1829
QY	459	ArgSerAlaGly---TyrThrProLeuLysValAsnGlyValGluTyrGlyGluThrArg	477
DB	1830	GAGTCCCGGAGCTGTACACCTCAGCTGAAGATGGCATTAAGGTCGGGAGGTCAAG	1889
QY	478	GluTyrGlyAsnPheSerPheThrArgValTyrGluAlaGlyHisGluValProTyrTyr	497
DB	1890	AATGCTGGCAAGTTTCACTTGTCTAGAAATGTTTGTGGAGGACACATGGTTTCCATACGAC	1949
QY	498	GlnProIleAlaSerLeuGlnLeuPheAsnArgThrIlePheGlyTyrAspIleAlaGlu	517
DB	1950	CAGCTGAGAGCTCTTGGCTATGCTGATGATGGAATGAGTGTGT---GACTACTCCTTG	2006
QY	518	GlyGlnLysLys	521
DB	2007	GGAACCAAGAA	2018

RESULT 6

US-10-369-493-36920

; Sequence 36920, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIOR FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 36920
 ; LENGTH: 1289
 ; TYPE: DNA
 ; ORGANISM: Aspergillus nidulans
 US-10-369-493-36920

Alignment Scores:
 Pred. No.: 6,14e-54 Length: 1289
 Score: 539.00 Matches: 149
 Percent Similarity: 44.86% Conservative: 69
 Best Local Similarity: 30.66% Mismatches: 171
 Query Match: 18.09% Indels: 98
 DB: 16 Gaps: 18

US-09-712-338-2 (1-555) x US-10-369-493-36920 (1-1289)

QY 65 ProGlyValIysSerTyrSerGlyTyrValAspThrSerProGluSerHisThrPhePhe 84
 Db 10 CCCGATGCAAGCAATACACGGGTATCTGGATGACAAATGAAATGATAA-ACATTGTT 68
 QY 85 -----Tip 85
 Db 69 TTACTGTAAGTTGATATTGTCGTGATGGGAGAGTAATATATAACGAGCTGAAGGG 128
 QY 86 PhePheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsnGlyGly 105
 Db 129 TTCCTTGAGTCAGCAACGACCCCAAAACGATCCTGTGTTCTGTGTTGAAACGGTGGC 188
 QY 106 ProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHisValAsnSer 125
 Db 189 CCTGGCTGTTCTTCTCTCACTGGACTCTTCATGGAGCTTGGGCCAGCAGTAATTGATGAG 248
 QY 126 ThrPheAspThrIleAsnProHisSerTyrAsnGluValSerAsnLeuLeuPheLeu 145
 Db 249 AACATCAAGCCGGTTTATACCCGTATGCGTGGAACTCCCAACGCTTCCGTTATCTCTTG 308
 QY 146 SerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIleAsnPro 165
 Db 309 GACCAGCCGTCACAGTTGCTACTCTTACG----- 341
 QY 166 ValThrGlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrProThrIle 185
 Db 341 ----- 341
 QY 186 AspAlaThrLeuIleAspThrAsnLeuAlaGluAlaTrpGluIleLeuGln 205
 Db 342 GGCAGTACTCTCAGCAGACTGTT---GCTGCTGGAAGGACGTTTACGCCCTTGCTTACT 398
 QY 206 GlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPheSerLeu 225
 Db 399 CTGTTCTTCAAGCAATTCCT-----GAGTATCCGAGCAGGAGTTTCCACATC 446
 QY 226 TrpThrGluSerTyrGlyHisTyrGlyProAlaPheAsnHisPheTyrGluGln 245
 Db 447 GCTGGAGAAATCTATGTCGCCACTACATTCTGTTTACTTCTGAGATCCTCTCTCAC 506
 QY 246 AsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSerLeuGly 265
 Db 507 CAGAAGCGC-----AACATCAACCTGAAGTCCGTCCTTA 539

QY 266 IleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPheAlaVal 285
 Db 540 ATCGCAACGGCTTGACCGGAGCTCTACCCAGTACGAATACTACCGCCCATGCGCTGT 599
 QY 286 AsnAsnThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLysPheAla 305
 Db 600 GCGCAGGGT---GGCTATCTGCTGCTGGATGAG-----AGCAGCTGC 641
 QY 306 AsnGlnMetProAsnGly-----CysGlnAspLeuIleSerThrCysLysGlnThr 322
 Db 642 CGCTCCATGGACAATGCTCTTGGTCGATGCGAGTCTATGATTGATCTTGTCTCAACAGT 701
 QY 323 AsnArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAsp 342
 Db 702 GAGAGTGCT-----TGGTCTGTGTCGCCGCTCCATATATCTGTAAACAAC 746
 QY 343 AsnValGluGlyProTyrTyrAlaPheAlaGlyGlyValTyrAspIleArgHisPro 362
 Db 747 GCCTCTCTCGCTCTTATCAGCGC---ACCGGACAGAACGTGTACGAGCTTCGGGGCAG 803
 QY 363 TyrAspAspProThr-----ProProSerTyrTyrAsnLysPheLeuAla 377
 Db 804 TCGGAGCAGCAGAGTAACCTTTGTTACAAAGGTATGGTTACGTTTCCGAATATCTGAC 863
 QY 378 LysAspSerValMetAspAlaIleGlyValAsnIleAsn---TyrThrGlnSerAsnAsn 396
 Db 864 AAGCTGAAGTCCGTGCGGCTGCGGTGCGGAGGTGATGTTTACGACTCTCTGCAATTT 923
 QY 397 AspValTyrTyrAlaPheGlnThrGlyAspPheValTrpPro-----AsnPheIle 414
 Db 924 GACATCAACCGCACTCTCTCCATGGTGTGATCGGATGAACCTTACACCGCTTGTGTC 983
 QY 415 GluAspLeuGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAsp 433
 Db 984 CTGGCATCTTTCAG-----CAGATACCTGTT-----CTCATCTATGCTGTGAT 1028
 QY 434 AlaAspTyrIleCysAsnTrpPheGlyGlyAlaValSerLeuAlaAlaAsnTyrSer 453
 Db 1029 GCGAATTCATCTGCAACTGGCTCGGAAACAAAGCCCTGGAGCTTGAATGCGCT 1088
 QY 454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysVal----- 468
 Db 1089 GGCACACAGGAGTTCGCCGAGCTCCCATGAGAGATCTAAAGATCTGCGACAGAACAC 1148
 QY 469 AsnGlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyr 488
 Db 1149 ACTGCAAGAAAGATCGCCAGATCAAGCCCATGGCAACTTCACTTTCATGCGCTCTAT 1208
 QY 489 GluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArg 508
 Db 1209 GTGGCGGCCACATGTTCCCATGAGCCAGCTGAGGCACTCCCTTGATGTTCTTCAACCGC 1268
 QY 509 ThrIlePheGly---Trp 513
 Db 1269 TGCTGGTGGCGAGTGG 1286

RESULT 7

US-10-369-493-27598
 ; Sequence 27598, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 27598

; LENGTH: 1619

; TYPE: DNA

; ORGANISM: Neurospora crassa

US-10-369-493-27598

Alignment Scores:

Pred. No.: 9.24e-53 Length: 1619
 Score: 530.50 Matches: 154
 Percent Similarity: 43.91% Conservative: 66
 Best Local Similarity: 30.74% Mismatches: 187
 Query Match: 17.81% Indels: 95
 DB: 16 Gaps: 18

US-09-712-338-2 (1-555) x US-10-369-493-27598 (1-1619)

Qy 47 AsnValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThrProGly 66
 Db 295 AACCTGCGCGTCAAGTCGTCGATCTCCAGCTCGCGTGCACAAG-----342
 Qy 67 ValLysSerTyrSerGlyTyrValAspThrSerPro---GluSerHisThrPhePheTrp 85
 Db 343 GTCAAGCAGTACAGCGGTTACCTTGATGACGAGGAGACGATAAGCACTGTTACTGTG- 401
 Qy 85 -----85
 Db 402 TAAGTCAATACGCTCGAATGATCTGTTAGTAAATACGCGTGCATCGGACGTGT 461
 Qy 86 -----PhePheGluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsn 103
 Db 462 CCAGGGTTCTTCGAGTCTCGCAACGATCCCAAGACGACCCGCTGTTTGTGGTTGAAC 521
 Qy 104 GlyGlyProGlySerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHisVal 123
 Db 522 GGTGCGCCCGGTGCTCTTCGTCACCTGCTCTCTTCCTTGAGCTCGGCGCTTCTTCCATT 581
 Qy 124 AsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeu 143
 Db 582 GACAAGAGCTCAGGGTGTGACGACGAGTACGCTTGACACCAACGCGCAGCGTTATC 641
 Qy 144 PheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIle 163
 Db 642 TTCCTTGACCGCCGCTCAAGCTCGGTACTCGTACTCC-----680
 Qy 164 AsnProValThrGlyValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrPro 183
 Db 680 -----680
 Qy 184 ThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaGluAlaAlaTrpGluIle 203
 Db 681 -----GGCAACGCCGTCGACACACTGTCGTCGCGCAAGAGATGTTATGCTCTC 731
 Qy 204 LeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPhe 223
 Db 732 CTTACCCCTCTCTCCACCAGTTCC-----GAGTATGCCAAGCAGGACTTC 779
 Qy 224 SerLeuTrpThrGluSerTyrGlyHisTyrGlyProAlaPhePheAsnHisPheTyr 243
 Db 780 CACATTGTCGGGAGCTTATGTCGTGCTACTACCTCTGCTTTCGAGATCTTG 839
 Qy 244 GluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSer 263
 Db 840 TCCACAGGATCGC-----AACATCAATCTCAAGTCC 872
 Qy 264 LeuGlyIleIleAsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPhe 283
 Db 873 GTCCTTATGGTAATGGCTTGAATGATGATCTCTTACCCGATGACGACTACCGCCCGC 932
 Qy 284 AlaValAsnAsnThrTyrGlyIleIleAlaValAsnGluThrValTyrAsnTyrMetLys 303
 Db 933 GCCTCGCGCAAGGTGGCTACCCCGCGCTTCTCAGCGAGGAGGTGCGCGACATGGAC 992

Qy 304 PheAlaAsnGlnMetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsn 323
 Db 993 -----AATGCCCTCCCGAGA---TGCAGTCTCTTATCCGTAAGTCTGCTAGAGAGC--- 1040
 Qy 324 ArgThrAlaLeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsn 343
 Db 1041 -----GGCAGTGTCTGCTGCTGCTCTCTCGCGCATCTACTGTAAACAATCAG 1088
 Qy 344 ValGluGlyProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisProTyr 363
 Db 1089 TTCATCGCGCCCTTACCAGCGC---ACTGGTCAGAACCTCTATGACATCCCGTGGAAAGTGC 1145
 Qy 364 AspAspProThrProProSerTyr-----TyrAsnLysPheLeuAlaLys 378
 Db 1146 GAGGATGATAGCAACCTCTGCTATAGCGCTTGGCTGGATCAGGACTACTCTGAACACAG 1205
 Qy 379 AspSerValMetAspAlaIleGlyValAsnIle---AsnTyrThrGlnSerAsnAsp 397
 Db 1206 AAGGATGTGATGAGCGCTCTCGCGCTCGAGGTTGAGGCTATGAGAGCTGCAACTTTGAT 1265
 Qy 398 ValTyrTyrAlaPheGlnGlnThrGlyAspPheValTrpProAsnPheIleGluAspLeu 417
 Db 1266 ATCAACCGCAACTTCTCTTCCAGGCTGACTGGATGACAGCCC---TTCATCGCCTCGTC 1322
 Qy 418 GluGluIleLeu---AlaLeuProValArgValSerLeuIleTyr---GlyAspAlaAsp 435
 Db 1323 CCGCGCATCTCAAGGAGATCCCGTT-----CTCATCTATCGCGTGATCGCGAC 1373
 Qy 436 TyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSerGlnAla 455
 Db 1374 TTCATCTGCAACTGCTCGCAACAAGGCTTGGAGCGAGGCTCTTGTAGTGGCCCGCGCAAG 1433
 Qy 456 AlaGlnPheArgSerAlaGlyTyrThrProLeuLysValAsnGlyVal-----GluTyr 473
 Db 1434 AACGGCTTCAACAGAGCTGAGCTCGAGGACCTCTCTTCTCCCAAGGCTGACAGGAGTAC 1493
 Qy 474 GlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGluAlaGlyHisGlu 493
 Db 1494 GGCAAGGTCAAGTCTCCGGAACCTTCACCTTCATGTCAGACTCTACAGGTTGGCCACATG 1553
 Qy 494 ValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArgThrIlePheGly--- 512
 Db 1554 GTGCCAATGGACCGCTGAGAACTCGTTCCTTCAACAGGTGTTGGCGGTGAA 1613
 Qy 513 Trp 513
 Db 1614 TGG 1616

RESULT 8

US-10-369-493-25613
 ; Sequence 25613, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xiaofeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 25613
 ; LENGTH: 1599
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-10-369-493-25613

Alignment Scores:

Pred. No.: 2,07e-52 Length: 1599
 Score: 527.50 Matches: 149
 Percent Similarity: 42.97% Conservatives: 71
 Best Local Similarity: 29.10% Mismatches: 195
 Query Match: 17.71% Indels: 97
 DB: 16 Gaps: 19

US-09-712-338-2 (1-555) x US-10-369-493-25613 (1-1599)

QY 33 ProLysAsnProThrGlyValIleThr-----LeuThrAlaAsnAsn 47
 DB 244 CCAAAATTCCTGAAGCAATCAAAACGAAGAAAGACTGGGACTTTGTGTCAAGAAATGAC 303
 QY 48 ValThrIleArgTyr-----LysGluProGlyAlaGluGlyVal 60
 DB 304 GCAATTGAAGAACTATCAGCTTCGTCTCAACAGATTAGGACCTTAAATCCTGGGCAT 363
 QY 61 CysGluThrThrProGlyValIleSerTyrSerGlyTyrValAspThrSerProGlu--- 79
 DB 364 -----GACCCAAATGTCAACAGTACACGGGTTACTTGGATGTGGAAGACGAGGAC 414
 QY 80 SerHisThrPheThrPheGluAlaArgHisAsnProGluThrAlaProIleThr 99
 DB 415 AAGCATTTCTTTTGGACTTTTGAAGTAGAAGCAATCTCGCAAGGATCCGGTCTATC 474
 QY 100 LeuTrpLeuAsnGlyProGlySerAspSerLeuIleGlyLeuPheGluGluGly 119
 DB 475 CTITGGTTGAACGGGGTCCAGGTTGTCTTCACTAACCGGGCTGTCTTTGAATTAGGA 534
 QY 120 ProCysHisValAsnSerThrPheAspAspTyrIleAsnProHisSerTrpAsnGluVal 139
 DB 535 CCTCATCCATTGGACCTGATTTGAACCCCATCGGAACCTTACTCTTGAACAGCAAT 594
 QY 140 SerAsnLeuLeuPheLeuSerGlnProLeuGlyValGlyPheSerTyrSerAspThrVal 159
 DB 595 GCCACCGTGATCTCTTGACCAACGCTGCAACGTTGGGTTCTCGTATTC- 645
 QY 160 AspGlySerIleAsnProValThrGlyValGluAsnSerSerPheAlaGlyValGln 179
 DB 646 -----GGTCTCTCA 654
 QY 180 GlyArgTyrProThrIleAspAlaThrLeuIleAspThrThrAsnLeuAlaGluAla 199
 DB 655 GGT-----GTTTCCAACACTGTCGCGCTGGTGAAGAT 687
 QY 200 AlaTrpGluIleLeuGlnGlyPheLeuSerGlyLeuProSerLeuAspSerArgValGln 219
 DB 688 GTCTATAACTTTTGGAGTTGTTCTTCGATCAGTTCCTCGAATACGTCACAAAGGGCCAA 747
 QY 220 SerLysAspPheSerLeuTrpThrGluSerTyrGlyGlyHisTyrGlyProAlaPhePhe 239
 DB 748 -----GATTTCACATCGCTGGGGAATCTACGCGGCATACATCCCTGTTTTGCC 801
 QY 240 AsnHisPheTyrGluGlnAsnGluArgIleAlaAsnGlySerValAsnGlyValGlnLeu 259
 DB 802 TCTGAAATTTTGTCTCAACAGGACAGA----- 828
 QY 260 AsnPheAsnSerLeuGlyIleIle-----AsnGlyIleIleAspGluAlaIleGlnAla 277
 DB 829 AACTTAACTTAACCTCCGCTTGTATCGGAATGGGCTCACTGACCCATTGACTCAGTAT 888
 QY 278 ProTyrTyrProGluPheAla-----ValAsnAsnThrTyr 289
 DB 889 AACTATTACCAACCAATGGCTGTGGTGAAGTGGGCAACCACTGTTTGGCCCTCGGAG 948
 QY 290 GlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLysPheAlaAsnGlnMetPro 309
 DB 949 GAATGCTCTGCTATGGAAGACTCTTTG----- 975
 QY 310 AsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsnArgThrAlaLeuAlaAsp 329
 DB 976 GAACGTTGTTGGCTTGTATCGATCGATCGTCTGCTACTCGCAA-----TCC 1020

QY 330 TyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsnValGluGlyProTyrTyr 349
 DB 1021 GTCTGGTCTGTGTCCAGCTTACCAATTTATTTGTAATAACGCCCAATTGGCTCTTACCACAA 1080
 QY 350 AlaPheAlaGlyArgGlyValTyrAspIleArgHisProTyrAspAsp----- 365
 DB 1081 CGT---ACCGGCAGAAAGCTTTACGATATACGGAAGGATTTGTAAGTGGCAATTTGTGC 1137
 QY 366 ---ProThrProSerTyrTyrAsnLysPheLeuAlaLysAspSerValMetAspAla 384
 DB 1138 TACCAACAGTTTACAAGAT---ATCGACGACTACTTAAACACGAGGACTACGTCAAAGAAGCT 1194
 QY 385 IleGlyValAsnIleAsnTyrThrGlnSer---AsnAsnAspValTyrTyrAlaPheGln 403
 DB 1195 GTCGGTGGGAGGTGACCACTACGAATCTCTGTAACCTTCGATATCAACAGAAATTTCTCTG 1254
 QY 404 GlnThrGlyAspPheValTrpProAsnPheIleGluAspLeuGluIleLeuAlaLeu 423
 DB 1255 TTTGCGGTGATTGGATGAAGCCT--TACCACACCGCCGTAACAGATCTTTTGAATCAA 1311
 QY 424 ProValArgValSerLeuIleTyrGlyAspAlaAspTyrIleCysAsnTrpPheGlyGly 443
 DB 1312 GACCTACCCATCTCTGGTATATGACAGCGGATAAAGATTTCATCTGTAATCTGGTAAAT 1371
 QY 444 GlnAlaValSerLeuAlaAlaAsnTyrSerGlnAlaGlnPheArgSer----- 460
 DB 1372 AAGCGGTGGACGGATGCTTGGCCATGGAAGTACGACGAAATTTGCAAGCCAAAGTA 1431
 QY 461 AlaGlyTyrThrProLeuLysValAsnGlyValGluTyrGlyGluThrArgGluTyrGly 480
 DB 1432 CGTAACCTGGACTGCTTCTATCATCCGACGAGTGCCT---GGTGAAGTCAATCTCTACAG 1488
 QY 481 AsnPheSerPheThrArgValTyrGluAlaGlyHisGluValProTyrTyrGlnProIle 500
 DB 1489 CACTTCACTATTGAGAGTCTTCAATGGTGGCCACATGTTCCATTTGACGTCCCTGAA 1548
 QY 501 AlaSerLeuGlnLeuPheAsnArgThrIlePheGly 512
 DB 1549 AAGCCTTAAGTATGTGTTAAAGAAATGATCCACCGT 1584

RESULT 9

US-10-425-114-6406
 ; Sequence 6406, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 6406
 ; LENGTH: 1751
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700563631_FLI
 ; US-10-425-114-6406

Alignment Scores:
 Pred. No.: 1,37e-46 Length: 1751
 Score: 479.50 Matches: 141
 Percent Similarity: 43.98% Conservatives: 93
 Best Local Similarity: 26.50% Mismatches: 219
 Query Match: 16.10% Indels: 79
 DB: 13 Gaps: 18

QY 10 LeuProLeuValAlaAlaSerTrpAlaLeuProGlySerThrProAlaSerValGlyArg 29
 Db 196 TTGCTCTCACTGCTGCG-----GAGGACCGGGGATGTTGAACGG 237
 QY 30 ArgGlnLeuProLysAsn-----ProThrGlyValLysThrLeuThrAlaAsnAsn 47
 Db 238 AAGTTCGTATTCCTCCGAATATATCTGCCGATGGTGGCCCTACTGTCGACGATTTAGGTCA 297
 QY 48 ValThrIleArgTyrLysGluProGlyAlaGluGlyValCysGluThrThrProGlyVal 67
 Db 298 CATGCTGTTATTACAGCTCCGAAATCTCGTGGC----- 333
 QY 68 LysSerTyrSerGlyTyrValAspThrSerProGluSerHisThrPhePheTrpPhe 87
 Db 334 -----GCAAGCATGTTCTACTCTCTCTC 357
 QY 88 GluAlaArgHisAsnProGluThrAlaProIleThrLeuTrpLeuAsnGlyGlyProGly 107
 Db 358 GAGTCACGG-----AACAAGAGGATGCTCTCTGTGTGATTTGGTTGACGGAGGGCTGGA 414
 QY 108 SerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHisValAsnSerThrPhe 127
 Db 415 TGTAGTAGTGAGTTGGCTGTGTTCTATGAGAAATGCTCTTCAAGATCACTAGTAACATG 474
 QY 128 AspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuLeuPheLeuSerGln 147
 Db 475 TCTCTGCTGGATGAGATGGATGGATGAGTTCCTCCATCTCTGTATGTTGATCAG 534
 QY 148 ProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIleAsnProValThr 167
 Db 535 CCTGTTGGAAGTGGTTTCAGCTACACACACATAAAGTGTATATCCGTCATGACGAACT 594
 QY 168 GlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrProThrIleAspAla 187
 Db 595 GGAGTT----- 600
 QY 188 ThrLeuIleAspThrThrAsnLeuAlaAlaGluAlaTrpGluIleLeuGlnGlyPhe 207
 Db 601 -----AGCAATGATCTTTATGATTTCTGCAGCGCTTC 633
 QY 208 LeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPheSerLeuTrpThr 227
 Db 634 TTTCGGGAGCACCTTAAGTTG-----GCAAAAAACGACTTTTATATTACTGGA 681
 QY 228 GluSerTyrGlyGlyHisTyrGlyProAlaPhePheAsnHisPheTyrGluInAsnGlu 247
 Db 682 GAGTCATATCTGGGCACTATATCCAGCTTTTCTCCGAGTCCATAAAGGAAACAAG 741
 QY 248 ArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSerLeuGlyIleIle 267
 Db 742 -----GCTAAT-----GAGGAGATTTCATATTAACTTAAGGATTCGCTATTGGA 786
 QY 268 AsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPheAlaValAsnAsn 287
 Db 787 AATGGGCTTACAGATCTGCACCTCAATACCCAGCTTATCTGACTACGCTTTGGAA--- 843
 QY 288 ThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLysPheAlaAsnGln 307
 Db 844 ---ATGGTCTAATACGCAAAAGAG-----CATGATCGCTTAGAAAAAGATT 888
 QY 308 MetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsnArgThrAla--- 326
 Db 889 GTCCCACTG---TGCGAATCAATCAATCAAGCTTTGTGGAATCTATGCGCAACTTCTGT 945
 QY 327 LeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsnValGluGly 346
 Db 946 TTGGCATCATATCTGTCTGCAACTCTTTGTCAGTGGTGAATGATGATGCTGTGGA 1005
 QY 347 ProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisPro----- 362
 Db 1006 GTAACATAT-----TACGATCATCAGGAAGAGTGCCTGGGAAGT 1044

QY 363 -----TyrAspAspProThrProSerTyrTyrAsnLysPheLeuAlaLysAspSer 380
 Db 1045 TTGTGCTACGATTC-----TCAACACATGGAGAAATTTTGAATCTGCAATCT 1092
 QY 381 ValMetAspAlaIleGlyVal---AsnIleAsnTyrThrGlnSerAsnAsnAspValTyr 399
 Db 1093 GTGAGGAAGTCACTTGTTGGTGGGACATACACTTTGTCTCTCGCAGTACTTCAGTCTAT 1152
 QY 400 TyrAlaPheGlnGlnThrGlyAspPheValTrpProAsnPheIleGluAsp----- 416
 Db 1153 CAGGCAATGCTGTAGAT-----TGGATGAGGAATCTCGAGGTTGGAATCCC 1200
 QY 417 -----LeuGluGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAsp 433
 Db 1201 ACGTCTTGGAGATGGAATCAGCCTC-----CTGTGTATGCTGGAGAA 1245
 QY 434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAlaAsnTyrSer 453
 Db 1246 TATGATCTTATCTGCACTGGCTCGTAACTCGAGTGGTGAATGCAATGGAATGGTCA 1305
 QY 454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysValAsnGlyValGluTyr 473
 Db 1306 GGGAAAAACAACTTTGGGGCGCTAAAGAGTTCCGTTTATTGTGGATGGCAAGAGCA 1365
 QY 474 GlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGluAlaGlyHisGlu 493
 Db 1366 GGCTTGTAAAGACTTATGAACTCACTCAGTTTCCTCAAGGTGAGAGATGCAGGACACATG 1425
 QY 494 ValProTyrTyrGlnIleAlaSerLeuGlnLeuPheAsnArg 508
 Db 1426 GTTCCATGACCGACGCTTAAGCTGCATGAAATGCTGAACGGA 1470

RESULT 11

US-09-938-842A-683
 ; Sequence 683, Application US/09938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 683
 ; LENGTH: 1551
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-683

Alignment Scores:

Pred. No.: 3,91e-46 Length: 1551
 Score: 475.00 Matches: 152
 Percent Similarity: 42.72% Conservative: 68
 Best Local Similarity: 29.51% Mismatches: 189
 Query Match: 15.94% Indels: 106
 DB: 11 Gaps: 20

US-09-712-338-2 (1-555) x US-09-938-842A-683 (1-1551)

QY 10 LeuProLeuValAlaAlaSerTrpAlaLeuProGlySerThrProAlaSerValGlyArg 29
 Db 196 TTGCTCTCACTGCTGCG-----GAGGACCGGGGATGTTGTAACGG 237

Qy 30 ArgGlnLeuProLysAsn-----ProThrGlyValLysThrLeuThrThrAlaAsnAsn 47
Db 238 AAGTTGCTATATCCCGAATATATCTTGGCGATGGTGGCCCTACTGTCGACGATTTAGGTCAT 297
Qy 48 ValThrIleArgTyrLysGluProGlyValAlaGluGlyValCysGluThrThrProGlyVal 67
Db 298 CATGCTGGTTATTACAGCTCCGAAATCTCGTGGC----- 333
Qy 68 LysSerTyrSerGlyTyrValAspThrSerProGluSerHisThrPhePheThrPhePhe 87
Db 334 -----GCAAGCATGTTCTACTTCTTCTC 357
Qy 88 GluAlaArgHisAsnProGluThrAlaProIleThrLeuThrLeuAsnGlyGlyProGly 107
Db 358 GAGTCACCG--AACAAAGAGAGTCTCTCTGTTGATTTGGTTGACGGGAGGCGCTGGA 414
Qy 108 SerAspSerLeuIleGlyLeuPheGluGluLeuGlyProCysHisValAsnSerThrPhe 127
Db 415 TGTAGTAGTAGTGGCTGTGTTCTATGAGATGCTCTTCAAGATCACTAGTAACATG 474
Qy 128 AspAspTyrIleAsnProHisSerTrpAsnGluValSerAsnLeuLeuPheLeuSerGln 147
Db 475 TCTCTGTCTTGAATGAGTATGATGGATCAGGTTTCCAAATCTTCTGTATGTTGATCAG 534
Qy 148 ProLeuGlyValGlyPheSerTyrSerAspThrValAspGlySerIleAsnProValThr 167
Db 535 CCTGTGTGAACCTGGTTTTCAGCTACACGACAGATAAAAGTGATATCCGTCATGACGAAACT 594
Qy 168 GlyValValGluAsnSerSerPheAlaGlyValGlnGlyArgTyrProThrIleAspAla 187
Db 595 GGAGTT----- 600
Qy 188 ThrLeuIleAspThrThrAsnLeuAlaGluAlaAlaTrpGluIleLeuGlnGlyPhe 207
Db 601 -----AGCAATGATCTTTATGATTTTCTGCGAGCTTTC 633
Qy 208 LeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPheSerLeuThr 227
Db 634 TTTGGCGACACCTTAAGTTG-----GCAAAACGACCTTTATATTTACTGGA 681
Qy 228 GluSerTyrGlyGlyHisTyrGlyProAlaPhePheAsnHisPheTyrGluGlnAsnGlu 247
Db 682 GAGTATATCTGGGCACTATATCCAGCTTTTGTCTCCGAGTCCATAAAGAAACAAAG 741
Qy 248 ArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSerLeuGlyIleIle 267
Db 742 -----GCTAAT-----GAGGAGTTCATATTAACTAAAGGGATTCGCTATTGGA 786
Qy 268 AsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPheAlaValAsnAsn 287
Db 787 AATGGGCTTACGATCCTGACCTCCAAATACCAGCCTATCCGACTACCTTTGGAA--- 843
Qy 288 ThrTyrGlyIleLysAlaValAsnGluThrValTyrAsnTyrMetLysPheAlaAsnGln 307
Db 844 ---ATGGGTATATCAGCAAAAGAG-----CATGATCGCTTAGAAAAGATT 888
Qy 308 MetProAsnGlyCysGlnAspLeuIleSerThrCysLysGlnThrAsnArgThrAla--- 326
Db 889 GTCCCACTG---TGCGAACTATCAATCAAGCTTTTGTGGAACCTGATGGCAACAACCTCTG 945
Qy 327 LeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsnValGluGly 346
Db 946 TTGGCATCATATCTTGCTGCAACTCTTTGTCAGTGGGTGTAATGATGATGCTGCTGGA 1005
Qy 347 ProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisPro----- 362
Db 1006 GTAAACTAT-----TACGACATCAGGAAGAAGTGCCTGGGAAGT 1044
Qy 363 -----TyrAspAspProThrProProSerTyrTyrAsnLysPheLeuAlaLysAspSer 380
Db 1045 TTGTGCTACCATTTTC-----TCAACATGAGAGAAATTTTGAATCTGCAATCT 1092
Qy 381 ValMetAspAlaIleGlyVal---AsnIleAsnTyrThrGlnSerAsnAspValTyr 399

Db 1093 GTGAGGAGTCACTTGGTGGGACATAGACTTTGCTCTCTCGACTACTTCAGTCTAT 1152
Qy 400 TyrAlaPheGlnGlnThrGlyAspPheValTyrProAsnPheIleGluAsp----- 416
Db 1153 CAGCAATGCTTGTAGAT-----TGGATGAGGAATCTCGAGGTTGGAATTCCTCC 1200
Qy 417 -----LeuGluGluIleLeuAlaLeuProValArgValSerLeuIleTyr---GlyAsp 433
Db 1201 ACGCTCTTGAAGATGAATCAGCTC-----CTTGTATGCTGGAGAA 1245
Qy 434 AlaAspTyrIleCysAsnTrpPheGlyGlyGlnAlaValSerLeuAlaAsnTyrSer 453
Db 1246 TATGATCTTATCTCAACTGCTGTAACCTCGAGTGGGTGAATGCAATGAGTGGTCA 1305
Qy 454 GlnAlaAlaGlnPheArgSerAlaGlyTyrThrProLeuLysValAsnGlyValGluTyr 473
Db 1306 GGGAAACAAACTTTGGGGCGCTAAAGAGTTCCTGTTTATGTGGATGGCAAGAACGA 1365
Qy 474 GlyGluThrArgGluTyrGlyAsnPheSerPheThrArgValTyrGluAlaGlyHisGlu 493
Db 1366 GCGTTGTTAAAGACTTATGAACAACCTCACTTCTCAAGTGCAGAGATGCAGGACACATG 1425
Qy 494 ValProTyrTyrGlnProIleAlaSerLeuGlnLeuPheAsnArg 508
Db 1426 GTTCAATGGACACGCTAAAGTGCATTTGAATGCTGAAGCGA 1470

RESULT 12
US-10-425-114-11176
; Sequence 11176, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yinhua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11176
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701038279_FLI
US-10-425-114-11176

Alignment Scores:
Pred. No.: 9,03e-46 Length: 1855
Score: 473.00 Matches: 133
Percent Similarity: 45.06% Conservative: 77
Best Local Similarity: 28.54% Mismatches: 182
Query Match: 15.88% Indels: 74
DB: 13 Gaps: 17

US-09-712-338-2 (1-555) x US-10-425-114-11176 (1-1855)
Qy 62 GluThrThrProGlyValLysSer-----TyrSerGlyTyr-----ValAspThr 76
Db 359 GATTCGAGCCTTCGTTGAGGATTGGGTCCACCAGCTGGCTATTACCCCATTCAGCAT 418
Qy 77 SerProGluSerHisThrPhePheThrPhePheGluAlaArgHisAsnProGluThrAla 96
Db 419 TCACATGCCGCAAGGATGTTCTACTTTTCTTCGATCAGCAATAGGAAGGAGGAT--- 475
Qy 97 ProIleThrLeuThrLeuAsnGlyGlyProGlySerAspSerLeuIleGlyLeuPheGlu 116
Db 476 CCTGTGCTAATTTGGTTTGACTGGGGGACCTGGGTGTAGCAGTGAATGGCTTGTGTTTAT 535


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QY 467 LysValAsnGlyValGluTyrGlyGluThrArgGluTyrGlyAsnPheSerPheThrArg 486
Db 1442 GTTCTTTGATGATCAGAAAGCCGGATTACTCAAGAGCTATGACCTCTAAAGTTTCTTTAAG 1501
QY 487 ValTyrGluAlaGlyHisGluValProTyrTyrGlnProIleAlaSerLeuGlnLeuPhe 506
Db 1502 GTCCATAATGCGGGTCACATGGTTCCAAATGACACGCCCAAGGCTGCATTAGAGATGCTG 1561
QY 507 AsnArgThrIlePheGly 512
Db 1562 AAGAAAGTGGATTAAATGGA 1579

RESULT 13
US -10-437-963-52572
; Sequence 52572, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Bing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 52572
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54856C.1
US -10-437-963-52572

Alignment Scores:
Pred. No.: 3,58e-45 Length: 2018
Score: 468.50 Matches: 151
Percent Similarity: 41.94% Conservativeness: 78
Best Local Similarity: 27.66% Mismatches: 205
Query Match: 15.73% Indels: 113
DB: 17 Gaps: 20

US-09-712-338-2 (1-555) x US-10-437-963-52572 (1-2018)

QY 8 SerValLeuProLeuValAlaAlaSerTrpAlaLeuProGlySerThrProAla----- 25
Db 168 TCCGCTCCCTCCACCGCTCGGACCTCCCGTCCCGCGGGGAGGCTCCCGCTCGCGG 227
QY 26 -----SerValGlyArgArgGlnLeuProLysAsnProThrGly 38
Db 228 CCGTCGGCTCATCCGCGCGCTCAACCTCACCCCGGGAGCGCTCCCGCTCCCGCTCCA 287
QY 39 ValLysThrLeuThrThrAlaAsnAsnValThrIleArgTyrLysGluProGlyAlaGlu 58
Db 288 GCGCGGGTGTATGCGAGCGTCCCG-----CCGGAACCTTAGTCGAGA 329
QY 59 Gly-----Val 60
Db 330 GCGCCCATCCCTCGCCTCATGCGCACCGGGAGAGCGGGGCTCGTCTCGGTGAAGACC 389
QY 61 CysGluThrThrProGlyValLysSerTyrSerGlyTyrValAspThrSerProGluSer 80
Db 390 TCGGCCACACCGCGGGTACTACCGCC-----TCCCCAAC-ACC 427
QY 81 His-----ThrPhePheTrpPheGluAlaArgHisAsnPro---GluThrAla 96
Db 428 CACGACGCAAGGCTGTTTACTTCTTCTCGGCTCGCGGAGACGCGGACGCGGACGCG 487

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382 TCACGA---AATAGCAAAAGGACCCCTGTTGTAATCTGTTGACTGGAGGCCAGGGTGT 438
Qy Aspartic acid
Db 109 Aspartic acid
Db 439 AGTAGTGAATGGCTTTGTTTATGAAATGGTCTTTTACCATTTGCTGGAACATGTCT 498
Qy Aspartic acid
Db 129 Aspartic acid
Db 499 CTTATTGGATCAGATGGTGGACATCAACCTCTGTATGTGGACCAACCC 558
Qy Leucine
Db 149 Leucine
Db 559 ATTGTCACCGCTTTAGTTATAGT----- 582
Qy Valine
Db 169 Valine
Db 583 -----TCTGATGAGAGGACATTCGTCTAATGAAGATGAAGTTAGCAACGAC 630
Qy Leucine
Db 189 Leucine
Db 631 CTATATGAC-----TTCCTACAGCATCTCTTT 657
Qy Serine
Db 209 Serine
Db 658 GCTGAACACCCCTGAGTTT-----GAAAGAAATGACTTTTATATAACTGGAGAA 705
Qy Serine
Db 229 Serine
Db 706 TCATATGCTGGCCTACATTCCTGCTGCGGAGTCCACCAAGGAACAA--- 762
Qy Isoleucine
Db 249 Isoleucine
Db 763 -----GCTAAGATGGAATTCATATAACCTAAGAGGATTTGCTATTGCTAAT 810
Qy Glycine
Db 269 Glycine
Db 811 GGCCTGAGTACCCCTGCAATCAGTATAAAGCTTACACAGATTTGCTTTGGAC----- 864
Qy Tyrosine
Db 289 Tyrosine
Db 865 -----ATGGGGGTAATTAAGAGTCTGACTACATCGTATC-----AACAAGCTG 909
Qy Proline
Db 309 Proline
Db 910 GTTCCAGTTGTTGAAATGCGAATTAAGCTTTGTGCACTGATGGCACAACTCTTGTGATG 969
Qy Alanine
Db 328 Alanine
Db 970 GCTTCATATTTGCTGTC-----AATGCCATATTCACTGGC 1005
Qy Tyrosine
Db 348 Tyrosine
Db 1006 ATCATGGCAGCTGTTGGCGATACAAATTTACTACGACATTTAGAACAAATGTGAAGGGAGC 1065
Qy Threonine
Db 367 Threonine
Db 1066 CTTTGCTATGACTCTCAACATGAGACATTTCTGAACAGGAAATCTGTAGGATGCC 1125
Qy Isoleucine
Db 385 Isoleucine
Db 1126 CTTGAGTTGGGATGATTGACTTTGTGCTGTCAGTCTACAGTGTATCAGGCCCATGCTG 1185
Qy Glutamine
Db 404 Glutamine
Db 1186 GTTGAC-----TGGATGAGGAATCTTGAAGTTGGCAITTCCTGCTCTCTCTGAG 1233
Qy Leucine
Db 423 Leucine
Db 1234 GATGGTCAAGCTTCTGTATGCTGGAGAAATATGATCTCATCTGCAACTGCTGCTGGC 1293
Qy Glycine
Db 443 Glycine
Db 1294 AATTGAGATGGTCTCATGCAATGGAATGGTCTGTCAGAGGAGTTTGTAGCATCTCTCT 1353

Qy Tyrosine
Db 1354 GAGGTCTCTTTGTCGTGTGATGGCTCAGAACAGGAGTCTTTGAGAACTCATGGACCTCTT 1413
Qy Serine
Db 483 Serine
Db 1414 GGTTCCTAAGGTTTCAGATGACGATGACATGTTCTTATGGACCAAGGACGCA 1473
Qy Leucine
Db 503 Leucine
Db 1474 TTGAGATGCTGAAGCGGTGAGCTAAGGCTACATTTATCTGAAGCTGCGGATTACAGAGAA 1533
Qy Lysine
Db 521 Lysine
Db 1534 TTGGTT 1539
RESULT 15
US-10-424-599-59411
; Sequence 59411, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 59411
; LENGTH: 1913
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2465C.1
US-10-424-599-59411
Alignment Scores:
Pred. No.: 1.5e-44 Length: 1913
Score: 463.00 Matches: 124
Percent Similarity: 44.93% Conservative: 80
Best Local Similarity: 27.31% Mismatches: 180
Query Match: 15.54% Indels: 70
DB: 13 Gaps: 15
US-09-712-338-2 (1-555) x US-10-424-599-59411 (1-1913)
Qy Tyrosine
Db 70 Tyrosine
Db 434 CATGAGGCTATTATCGCTTCCTCTCCAAAGCTGCAAGGATGTTCTACTTCTCTTT 493
Qy Glutamine
Db 88 Glutamine
Db 494 GAATCTCGA---AGCAGTAAGAAATGATCTGCTCATATGGCTGATGGAGGACCA 550
Qy Serine
Db 108 Serine
Db 551 TGCAGCAGTGAACATGCTTTTACGAAATGCTCTTTTACGCTTACCAAGAACTTG 610
Qy Aspartic acid
Db 128 Aspartic acid
Db 611 TCTCTTGTGGAATGACTATGCTGGACAGCATCAATATATATTTTGTAGACCAA 670
Qy Proline
Db 148 Proline
Db 671 CCCACTGGACGGGTTTCAGCTATCTGATGAGAGTGCACATTCGCCATGATGAAGAG 730
Qy Glycine
Db 168 Glycine
Db 731 GCGGTT----- 736

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QY 188 ThrLeuIleAspThrThrAsnLeuAlaAlaGluAlaAlaIleLeuGlnGlyPhe 207
Db      ::::: |||||
737 -----ACCAATGATTTGATCAGCTTTGAGGCAATTT 769
QY 208 LeuSerGlyLeuProSerLeuAspSerArgValGlnSerLysAspPheSerLeuThrThr 227
Db      ||| |||||
770 TTCAAGGAGCACCT-----CAATTCACCTAAGATGACCTTTATATTAAGTGA 817
QY 228 GluSerTyrGlyGlyHisTyrGlyProAlaPheAsnHisPheTyrGluGlnAsnGlu 247
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
818 GAGTCATATGCTGGACATTCACATTCAGCTCTTGATCCAGGGTTCACCAAGAAACAAA 877
QY 248 ArgIleAlaAsnGlySerValAsnGlyValGlnLeuAsnPheAsnSerLeuGlyIleIle 267
Db      ::::: |||||
878 -----GCAAAAGAGGAATTCATATAAATCTAAAGGATTTGCTATTGGT 922
QY 268 AsnGlyIleIleAspGluAlaIleGlnAlaProTyrTyrProGluPheAlaValAsnAsn 287
Db      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
923 AATGGTTTAAACCAATCTGAAATTCAGTACCAAGGGGTATACAGACTACGCATTAGACAGG 982
QY 288 ThrTyrGlyIleLeuAlaValAsnGluThrValTyrAsnTyrMetLysPheAlaAsnGln 307
Db      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
983 -----GGACTA-----ATTAAAGGCTGAATATACAGTATC-----AACAG 1021
QY 308 MetProAsnGlyCysGlnAspLeuIleSerThrCys---LysGlnThrAsnArgThrAla 326
Db      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1022 TTGATCCCAACCATGCAAGCAGCCATAGAAGCTTCGGAACTGGAAGTGGAGAACATGC 1081
QY 327 LeuAlaAspTyrAlaLeuCysAlaGluAlaThrAsnMetCysArgAspAsnValGluGly 346
Db      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1082 GTATCTCATATATATGTTTGCATAAGATATTCAATCGGATCATGACCATTCGTGTATGAT 1141
QY 347 ProTyrTyrAlaPheAlaGlyArgGlyValTyrAspIleArgHisPro----- 362
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1142 GTTATTAC-----TATGACATTAGAAAGAAATGTGTGGGAGTT 1180
QY 363 -----TyrAspAspProThrProSerTyrTyrAsnLysPheLeuAlaLysAspSer 380
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1181 CRGTGTATGACTTC-----TCTGTGTGGAGGATTTCTTAAACGAGAGACACA 1228
QY 381 ValMetAspAlaIleGlyVal---AsnIleAsnTyrThrGlnSerAsnAsnAspValTyr 399
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1229 GTGAGAGATGCTTTAGGTGTTGGGACTTGGACTTCGTTTCATGCAGTAGCACAGTGTAT 1288
QY 400 TyrAlaPheGlnGlnThrGlyAspPheValTyrProAsnPheIleGlu---AspLeuGlu 418
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1289 AGTGTATGATCAAGAC-----TGGATGAGAAATCTGGAAGTTGTTATTCCTCC 1336
QY 419 GluIleLeuAlaLeuProValArgValSerLeuIleTyrGlyAspAlaAspTyrIleCys 438
Db      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1337 ACACCTCTTGGGAAGGAATCAAGTGTGTGTATGCTGGAGAGAGAGATCTCATATGC 1396
QY 439 AsnTyrPheGlyGlyAlaValSerLeuAlaAlaAsnTyrSerGlnAlaIleGlnPhe 458
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1397 AATTGGCTTGGGAATCAAGTGGGTTCAGCAATGAGTGGTCTGCTCAAAACAAATTT 1456
QY 459 ArgSerAlaGlyTyrThrProLeuLysValAsnGlyValGluTyrGlyLeuThrArgGlu 478
Db      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1457 GGGGCGTCTGTACAGTCCCATTTTGGTTGATGTTGCTGAGCAGGACGCTGAAAAGC 1516
QY 479 TyrGlyAsnPheSerPheThrValTyrGluAlaGlyHisGluValProTyrTyrGln 498
Db      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1517 CATGGACCTCTCGCTTTCTCAAGGTATACAGGCTGCTGATGCTGCTGCTGATGATCAA 1576
QY 499 ProIleAlaSerLeuGlnLeuPheAsnArgThrIlePheGly 512
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1577 CCAAAAGCTGCATCTGAGATGCTAAGAGCTGGATGCAAGGC 1618
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Search completed: July 29, 2004, 13:49:59

Job time : 723 secs